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(57) Abstract: The present invention is directed to compositions of matter useful for the diagnosis and treatment of tumor in mammals and to methods of using those compositions of matter for the same.

COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

FIELD OF THE INVENTION

The present invention is directed to compositions of matter useful for the diagnosis and treatment of tumor in mammals and to methods of using those compositions of matter for the same.

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BACKGROUND OF THE INVENTION

Malignant tumors (cancers) are the second leading cause of death in the United States, after heart disease (Boring et al., CA Cancel J. Clin. 43:7 (1993)). Cancer is characterized by the increase in the number of abnormal, or neoplastic, cells derived from a normal tissue which proliferate to form a tumor mass, the invasion of adjacent tissues by these neoplastic tumor cells, and the generation of malignant cells which eventually spread via the blood or lymphatic system to regional lymph nodes and to distant sites via a process called metastasis. In a cancerous state, a cell proliferates under conditions in which normal cells would not grow. Cancer manifests itself in a wide variety of forms, characterized by different degrees of invasiveness and aggressiveness.

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In attempts to discover effective cellular targets for cancer diagnosis and therapy, researchers have sought to identify transmembrane or otherwise membrane-associated polypeptides that are specifically expressed on the surface of one or more particular type(s) of cancer cell as compared to on one or more normal non-cancerous cell(s). Often, such membrane-associated polypeptides are more abundantly expressed on the surface of the cancer cells as compared to on the surface of the non-cancerous cells. The identification of such tumor-associated cell surface antigen polypeptides has given rise to the ability to specifically target cancer cells for destruction via antibody-based therapies. In this regard, it is noted that antibody-based therapy has proved very effective in the treatment of certain cancers. For example, HERCEPTIN® and RITUXAN® (both from Genentech Inc., South San Francisco, California) are antibodies that have been used successfully to treat breast cancer and non-Hodgkin's lymphoma, respectively. More specifically, HERCEPTIN® is a recombinant DNA-derived humanized monoclonal antibody that selectively binds to the extracellular domain of the human epidermal growth factor receptor 2 (HER2) proto-oncogene. HER2 protein overexpression is observed in 25-30% of primary breast cancers. RITUXAN® is a genetically engineered chimeric murine/human monoclonal antibody directed against the CD20 antigen found on the surface of normal and malignant B lymphocytes. Both these antibodies are recombinantly produced in CHO cells.

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In other attempts to discover effective cellular targets for cancer diagnosis and therapy, researchers have sought to identify (1) non-membrane-associated polypeptides that are specifically produced by one or more particular type(s) of cancer cell(s) as compared to by one or more particular type(s) of non-cancerous normal cell(s), (2) polypeptides that are produced by cancer cells at an expression level that is significantly higher than that of one or more normal non-cancerous cell(s), or (3) polypeptides whose expression is specifically limited

to only a single (or very limited number of different) tissue type(s) in both the cancerous and non-cancerous state (e.g., normal prostate and prostate tumor tissue). Such polypeptides may remain intracellularly located or may be secreted by the cancer cell. Moreover, such polypeptides may be expressed not by the cancer cell itself, but rather by cells which produce and/or secrete polypeptides having a potentiating or growth-enhancing effect on cancer cells. Such secreted polypeptides are often proteins that provide cancer cells with a growth advantage over normal cells and include such things as, for example, angiogenic factors, cellular adhesion factors, growth factors, and the like. Identification of antagonists of such non-membrane associated polypeptides would be expected to serve as effective therapeutic agents for the treatment of such cancers. Furthermore, identification of the expression pattern of such polypeptides would be useful for the diagnosis of particular cancers in mammals.

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Despite the above identified advances in mammalian cancer therapy, there is a great need for additional diagnostic and therapeutic agents capable of detecting the presence of tumor in a mammal and for effectively inhibiting neoplastic cell growth, respectively. Accordingly, it is an objective of the present invention to identify: (1) cell membrane-associated polypeptides that are more abundantly expressed on one or more type(s) of cancer cell(s) as compared to on normal cells or on other different cancer cells, (2) non-membrane-associated polypeptides that are specifically produced by one or more particular type(s) of cancer cell(s) (or by other cells that produce polypeptides having a potentiating effect on the growth of cancer cells) as compared to by one or more particular type(s) of non-cancerous normal cell(s), (3) non-membrane-associated polypeptides that are produced by cancer cells at an expression level that is significantly higher than that of one or more normal noncancerous cell(s), or (4) polypeptides whose expression is specifically limited to only a single (or very limited number of different) tissue type(s) in both a cancerous and non-cancerous state (e.g., normal prostate and prostate tumor tissue), and to use those polypeptides, and their encoding nucleic acids, to produce compositions of matter useful in the therapeutic treatment and diagnostic detection of cancer in mammals. It is also an objective of the present invention to identify cell membrane-associated, secreted or intracellular polypeptides whose expression is limited to a single or very limited number of tissues, and to use those polypeptides, and their encoding nucleic acids, to produce compositions of matter useful in the therapeutic treatment and diagnostic

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SUMMARY OF THE INVENTION

A. Embodiments

detection of cancer in mammals.

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In the present specification, Applicants describe for the first time the identification of various cellular polypeptides (and their encoding nucleic acids or fragments thereof) which are expressed to a greater degree on the surface of or by one or more types of cancer cell(s) as compared to on the surface of or by one or more types of normal non-cancer cells. Alternatively, such polypeptides are expressed by cells which produce and/or secrete polypeptides having a potentiating or growth-enhancing effect on cancer cells. Again alternatively, such polypeptides may not be overexpressed by tumor cells as compared to normal cells of the same tissue type, but rather may be specifically expressed by both tumor cells and normal cells of only a single or very limited

number of tissue types (preferably tissues which are not essential for life, e.g., prostate, etc.). All of the above polypeptides are herein referred to as <u>Tumor-associated Antigenic Target polypeptides</u> ("TAT" polypeptides) and are expected to serve as effective targets for cancer therapy and diagnosis in mammals.

Accordingly, in one embodiment of the present invention, the invention provides an isolated nucleic acid molecule having a nucleotide sequence that encodes a tumor-associated antigenic target polypeptide or fragment thereof (a "TAT" polypeptide).

In certain aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity, to (a) a DNA molecule encoding a full-length TAT polypeptide having an amino acid sequence as disclosed herein, a TAT polypeptide amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane TAT polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity, to (a) a DNA molecule comprising the coding sequence of a full-length TAT polypeptide cDNA as disclosed herein, the coding sequence of a TAT polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane TAT polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length TAT polypeptide amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In further aspects, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity, to (a) a DNA molecule that encodes the same mature polypeptide encoded by the full-length coding region of any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect of the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a TAT polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide(s) are disclosed herein. Therefore, soluble extracellular domains of the herein described TAT polypeptides are contemplated.

In other aspects, the present invention is directed to isolated nucleic acid molecules which hybridize to (a) a nucleotide sequence encoding a TAT polypeptide having a full-length amino acid sequence as disclosed herein, a TAT polypeptide amino acid sequence lacking the signal peptide as disclosed herein, an extracellular

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domain of a transmembrane TAT polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide amino acid sequence as disclosed herein, or (b) the complement of the nucleotide sequence of (a). In this regard, an embodiment of the present invention is directed to fragments of a full-length TAT polypeptide coding sequence, or the complement thereof, as disclosed herein, that may find use as, for example, hybridization probes useful as, for example, diagnostic probes, antisense oligonucleotide probes, or for encoding fragments of a full-length TAT polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-TAT polypeptide antibody, a TAT binding oligopeptide or other small organic molecule that binds to a TAT polypeptide. Such nucleic acid fragments are usually at least about 5 nucleotides in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a TAT polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the TAT polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which TAT polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such novel fragments of TAT polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the TAT polypeptide fragments encoded by these nucleotide molecule fragments, preferably those TAT polypeptide fragments that comprise a binding site for an anti-TAT antibody, a TAT binding oligopeptide or other small organic molecule that binds to a TAT polypeptide.

In another embodiment, the invention provides isolated TAT polypeptides encoded by any of the isolated nucleic acid sequences hereinabove identified.

In a certain aspect, the invention concerns an isolated TAT polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity, to a TAT polypeptide having a full-length amino acid sequence as disclosed herein, a TAT polypeptide amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane TAT polypeptide protein, with or without the signal peptide, as disclosed herein, an amino acid sequence encoded by any of the nucleic acid sequences disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated TAT polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid

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sequence identity, to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated TAT polypeptide without the N-terminal signal sequence and/or without the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the TAT polypeptide and recovering the TAT polypeptide from the cell culture.

Another aspect of the invention provides an isolated TAT polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the TAT polypeptide and recovering the TAT polypeptide from the cell culture.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cells comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli* cells, or yeast cells. A process for producing any of the herein described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides isolated chimeric polypeptides comprising any of the herein described TAT polypeptides fused to a heterologous (non-TAT) polypeptide. Example of such chimeric molecules comprise any of the herein described TAT polypeptides fused to a heterologous polypeptide such as, for example, an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, single-chain antibody or antibody that competitively inhibits the binding of an anti-TAT polypeptide antibody to its respective antigenic epitope. Antibodies of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies of the present invention may optionally be produced in CHO cells or bacterial cells and preferably induce death of a cell to which they bind. For diagnostic purposes, the antibodies of the present invention may be detectably labeled, attached to a solid support, or the like.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described antibodies. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli* cells, or yeast cells. A process for producing any of the herein described antibodies is further provided and comprises culturing host cells under conditions suitable for expression of the desired antibody and recovering the desired antibody from the cell culture.

In another embodiment, the invention provides oligopeptides ("TAT binding oligopeptides") which

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bind, preferably specifically, to any of the above or below described TAT polypeptides. Optionally, the TAT binding oligopeptides of the present invention may be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The TAT binding oligopeptides of the present invention may optionally be produced in CHO cells or bacterial cells and preferably induce death of a cell to which they bind. For diagnostic purposes, the TAT binding oligopeptides of the present invention may be detectably labeled, attached to a solid support, or the like.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described TAT binding oligopeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli* cells, or yeast cells. A process for producing any of the herein described TAT binding oligopeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired oligopeptide and recovering the desired oligopeptide from the cell culture.

In another embodiment, the invention provides small organic molecules ("TAT binding organic molecules") which bind, preferably specifically, to any of the above or below described TAT polypeptides. Optionally, the TAT binding organic molecules of the present invention may be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The TAT binding organic molecules of the present invention preferably induce death of a cell to which they bind. For diagnostic purposes, the TAT binding organic molecules of the present invention may be detectably labeled, attached to a solid support, or the like.

In a still further embodiment, the invention concerns a composition of matter comprising a TAT polypeptide as described herein, a chimeric TAT polypeptide as described herein, an anti-TAT antibody as described herein, a TAT binding oligopeptide as described herein, or a TAT binding organic molecule as described herein, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

In yet another embodiment, the invention concerns an article of manufacture comprising a container and a composition of matter contained within the container, wherein the composition of matter may comprise a TAT polypeptide as described herein, a chimeric TAT polypeptide as described herein, an anti-TAT antibody as described herein, a TAT binding oligopeptide as described herein, or a TAT binding organic molecule as described herein. The article may further optionally comprise a label affixed to the container, or a package insert included with the container, that refers to the use of the composition of matter for the therapeutic treatment or diagnostic detection of a tumor.

Another embodiment of the present invention is directed to the use of a TAT polypeptide as described herein, a chimeric TAT polypeptide as described herein, an anti-TAT polypeptide antibody as described herein, a TAT binding oligopeptide as described herein, or a TAT binding organic molecule as described herein, for the preparation of a medicament useful in the treatment of a condition which is responsive to the TAT polypeptide, chimeric TAT polypeptide, anti-TAT polypeptide antibody, TAT binding oligopeptide, or TAT

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binding organic molecule.

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B. Additional Embodiments

Another embodiment of the present invention is directed to a method for inhibiting the growth of a cell that expresses a TAT polypeptide, wherein the method comprises contacting the cell with an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, and wherein the binding of the antibody, oligopeptide or organic molecule to the TAT polypeptide causes inhibition of the growth of the cell expressing the TAT polypeptide. In preferred embodiments, the cell is a cancer cell and binding of the antibody, oligopeptide or organic molecule to the TAT polypeptide causes death of the cell expressing the TAT polypeptide. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and TAT binding oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet another embodiment of the present invention is directed to a method of therapeutically treating a mammal having a cancerous tumor comprising cells that express a TAT polypeptide, wherein the method comprises administering to the mammal a therapeutically effective amount of an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, thereby resulting in the effective therapeutic treatment of the tumor. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet another embodiment of the present invention is directed to a method of determining the presence of a TAT polypeptide in a sample suspected of containing the TAT polypeptide, wherein the method comprises exposing the sample to an antibody, oligopeptide or small organic molecule that binds to the TAT polypeptide and determining binding of the antibody, oligopeptide or organic molecule to the TAT polypeptide in the sample, wherein the presence of such binding is indicative of the presence of the TAT polypeptide in the sample. Optionally, the sample may contain cells (which may be cancer cells) suspected of expressing the TAT polypeptide. The antibody, TAT binding oligopeptide or TAT binding organic molecule employed in the method may optionally be detectably labeled, attached to a solid support, or the like.

A further embodiment of the present invention is directed to a method of diagnosing the presence of a tumor in a mammal, wherein the method comprises detecting the level of expression of a gene encoding a TAT polypeptide (a) in a test sample of tissue cells obtained from said mammal, and (b) in a control sample of known normal non-cancerous cells of the same tissue origin or type, wherein a higher level of expression of the

TAT polypeptide in the test sample, as compared to the control sample, is indicative of the presence of tumor in the mammal from which the test sample was obtained.

Another embodiment of the present invention is directed to a method of diagnosing the presence of a tumor in a mammal, wherein the method comprises (a) contacting a test sample comprising tissue cells obtained from the mammal with an antibody, oligopeptide or small organic molecule that binds to a TAT polypeptide and (b) detecting the formation of a complex between the antibody, oligopeptide or small organic molecule and the TAT polypeptide in the test sample, wherein the formation of a complex is indicative of the presence of a tumor in the mammal. Optionally, the antibody, TAT binding oligopeptide or TAT binding organic molecule employed is detectably labeled, attached to a solid support, or the like, and/or the test sample of tissue cells is obtained from an individual suspected of having a cancerous tumor.

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Yet another embodiment of the present invention is directed to a method for treating or preventing a cell proliferative disorder associated with altered, preferably increased, expression or activity of a TAT polypeptide, the method comprising administering to a subject in need of such treatment an effective amount of an antagonist of a TAT polypeptide. Preferably, the cell proliferative disorder is cancer and the antagonist of the TAT polypeptide is an anti-TAT polypeptide antibody, TAT binding oligopeptide, TAT binding organic molecule or antisense oligonucleotide. Effective treatment or prevention of the cell proliferative disorder may be a result of direct killing or growth inhibition of cells that express a TAT polypeptide or by antagonizing the cell growth potentiating activity of a TAT polypeptide.

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Yet another embodiment of the present invention is directed to a method of binding an antibody, oligopeptide or small organic molecule to a cell that expresses a TAT polypeptide, wherein the method comprises contacting a cell that expresses a TAT polypeptide with said antibody, oligopeptide or small organic molecule under conditions which are suitable for binding of the antibody, oligopeptide or small organic molecule to said TAT polypeptide and allowing binding therebetween.

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Other embodiments of the present invention are directed to the use of (a) a TAT polypeptide, (b) a nucleic acid encoding a TAT polypeptide or a vector or host cell comprising that nucleic acid, (c) an anti-TAT polypeptide antibody, (d) a TAT-binding oligopeptide, or (e) a TAT-binding small organic molecule in the preparation of a medicament useful for (i) the therapeutic treatment or diagnostic detection of a cancer or tumor, or (ii) the therapeutic treatment or prevention of a cell proliferative disorder.

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Another embodiment of the present invention is directed to a method for inhibiting the growth of a cancer cell, wherein the growth of said cancer cell is at least in part dependent upon the growth potentiating effect(s) of a TAT polypeptide (wherein the TAT polypeptide may be expressed either by the cancer cell itself or a cell that produces polypeptide(s) that have a growth potentiating effect on cancer cells), wherein the method comprises contacting the TAT polypeptide with an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, thereby antagonizing the growth-potentiating activity of the TAT polypeptide and, in turn, inhibiting the growth of the cancer cell. Preferably the growth of the cancer cell is completely inhibited. Even more preferably, binding of the antibody, oligopeptide or small organic molecule to the TAT polypeptide induces the death of the cancer cell. Optionally, the antibody is a monoclonal antibody, antibody fragment,

chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and TAT binding oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet another embodiment of the present invention is directed to a method of therapeutically treating a tumor in a mammal, wherein the growth of said tumor is at least in part dependent upon the growth potentiating effect(s) of a TAT polypeptide, wherein the method comprises administering to the mammal a therapeutically effective amount of an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, thereby antagonizing the growth potentiating activity of said TAT polypeptide and resulting in the effective therapeutic treatment of the tumor. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet further embodiments of the present invention will be evident to the skilled artisan upon a reading of the present specification.

BRIEF DESCRIPTION OF THE DRAWINGS

In the list of figures for the present application, specific cDNA sequences which are upregulated in certain tumor tissues as compared to their normal tissue counterparts are individually identified with a designation beginning with the letters "DNA" followed by a specific numerical designation. A full or partial length protein sequence that is encoded by a cDNA sequence identified and shown herein is individually identified with a designation beginning with the letters "PRO" followed by a specific numerical designation. Figures showing encoded amino acid sequences immediately follow the figure showing the cDNA sequence encoding that specific amino acid sequence. If start and/or stop codons have been identified in a cDNA sequence shown in the attached figures, they are shown in bold and underlined font.

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List of Figures

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Figure 736: DNA324098, XM_117264, gen.XM_010881 gen.XM_117264 Figure 772: DNA324115, XM_087069, Figure 737: PRO80807 gen.XM_087069 Figure 738A-B: DNA324099, XM_031626, Figure 773: DNA324116, XM_016625, gen.XM_031626 gen.XM_016625 Figure 739: PRO80808 Figure 774: PRO80820 Figure 740: DNA324100, XM_057664, Figure 775: DNA324117, XM_087068, gen.XM_057664 gen.XM_087068 Figure 741: DNA226428, NM_000251, Figure 776: DNA324118, XM_002674, gen.NM_000251 gen.XM_002674 Figure 742: PRO36891 Figure 777: DNA324119, XM_065884, Figure 743: DNA324101, XM_087211, gen.XM_065884 gen.XM_087211 Figure 778: PRO80823 Figure 744A-B: DNA275066, NM_000179, Figure 779A-B: DNA324120, XM_002739, gen.NM_000179 gen.XM_002739 Figure 745: PRO62786 Figure 780: DNA324121, XM_031596, Figure 746A-C: DNA270154, NM_003128, gen.XM_031596 gen.NM_003128 Figure 781: PRO61325 Figure 747: PRO58543 Figure 782: DNA324122, XM_031585, Figure 748: DNA324102, XM_087051, gen.XM_031585 gen.XM_087051 Figure 783: DNA324123, XM_031586, Figure 749: DNA324103, NM _002954, gen.XM_031586 gen.NM_002954 Figure 784: DNA324124, XM_018039, Figure 750: PRO62239 gen.XM_018039 Figure 751: DNA271060, NM_002453, Figure 785: DNA324125, NM_032822. gen.NM_002453 gen.NM_032822 Figure 752: PRO59384 Figure 786: PRO80827 Figure 753: DNA324104, XM_048088, Figure 787A-B: DNA324126, XM_096172, gen.XM_048088 gen.XM_096172 Figure 754: PRO80811 Figure 788A-B: DNA324127, XM_002727, Figure 755: DNA324105, XM_010886, gen.XM_002727 gen.XM_010886 Figure 789: DNA324128, NM_003124, Figure 756: PRO80812 gen.NM_003124 Figure 757: DNA324106, XM_045283, Figure 790: PRO80830 gen.XM_045283 Figure 791: DNA324129, XM_086980, Figure 758: PRO80813 gen.XM_086980 Figure 759: DNA324107, NM_006430, Figure 792: DNA227795, NM_006429. gen.NM_006430 gen.NM_006429 Figure 760: PRO80814 Figure 793: PRO38258 Figure 761A-B: DNA324108, NM_003400, Figure 794: DNA287167, NM_006636, gen.NM_003400 gen.NM_006636 Figure 762: PRO59544 Figure 795: PRO59136 Figure 763: DNA324109, XM_018301, Figure 796: DNA324130, NM_033046, gen.XM_018301 gen.NM_033046 Figure 764: DNA324110, NM_005917, Figure 797: PRO80832 gen.NM_005917 Figure 798: DNA324131, NM_133637, Figure 765: PRO4918 gen.NM_133637 Figure 766: DNA324111, XM_016843, Figure 799: PRO80833 gen.XM_016843 Figure 800: DNA324132, XM_035220. Figure 767: PRO80816 gen.XM_035220 Figure 768: DNA324112, XM_088638, Figure 801: DNA324133, NM_013247, gen.XM_088638 gen.NM_013247 Figure 769: PRO80817 Figure 802: PRO80835 Figure 770: DNA324113, XM_002647, Figure 803: DNA227528, NM_021103, gen.XM_002647 gen.NM_021103 Figure 771: DNA324114, XM_010881, Figure 804: PRO37991

Figure 805: DNA324134, XM_086920. gen.XM_087122 gen.XM_086920 Figure 840: PRO80853 Figure 806: DNA150725, NM_001747, Figure 841: DNA324154, XM_018540, gen.NM_001747 gen.XM_018540 Figure 807: PRO12792 Figure 842: DNA324155, XM_087040. Figure 808: DNA324135, NM_005911, gen.XM_087040 gen.NM_005911 Figure 843: DNA324156, NM_032212, Figure 809: PRO80837 gen.NM_032212 Figure 810: DNA324136, NM_032827. Figure 844: PRO80856 gen.NM_032827 Figure 845: DNA324157, XM_002217, Figure 811: PRO80838 gen.XM_002217 Figure 812: DNA324137, NM_017952. Figure 846: PRO80857 gen.NM_017952 Figure 847: DNA324158, NM_000576, Figure 813: PRO80839 gen.NM_000576 Figure 814: DNA227190, NM_006839, Figure 848: PRO65 gen.NM_006839 Figure 849: DNA324159, XM_086923, Figure 815: PRO37653 gen.XM_086923 Figure 816: DNA324138, XM_114215, Figure 850: DNA324160, XM _086925. gen.XM_114215 gen.XM_086925 Figure 817: DNA324139, XM_052989, Figure 851A-B: DNA324161, XM_114266, gen.XM_052989 gen.XM_114266 Figure 818: DNA324140, XM_049116, Figure 852: PRO80860 gen.XM_049116 Figure 853: DNA324162, XM_002704. Figure 819: PRO80842 gen.XM_002704 Figure 820A-B: DNA324141, XM_049108, Figure 854: DNA194740, NM_005291, gen.XM_049108 gen.NM_005291 Figure 821: PRO80843 Figure 855: PRO24028 Figure 822: DNA324142, XM_049113, Figure 856A-B: DNA324163, XM_114267, gen.XM_049113 gen.XM_114267 Figure 823: DNA324143, XM_002611, Figure 857: DNA324164, XM_034952, gen.XM_002611 gen.XM_034952 Figure 824A-B: DNA324144, XM_114247, Figure 858: DNA324165, XM_086950, gen.XM_114247 gen.XM_086950 Figure 825: DNA324145, NM_017789, Figure 859A-B: DNA255531, NM_017751. gen.NM_017789 gen.NM_017751 Figure 826: PRO80846 Figure 860: PRO50596 Figure 827: DNA324146, NM_001862, Figure 861: DNA324166, XM_017698, gen.NM_001862 gen.XM_017698. Figure 828: PRO80847 Figure 862: DNA324167, XM_030529, Figure 829: DNA324147, NM_005783, gen.XM_030529 gen.NM_005783 Figure 863: PRO80866 Figure 830: PRO80848 Figure 864: DNA275240, NM_005915. Figure 831A-B: DNA324148, XM_037108, gen.NM_005915 gen.XM_037108 Figure 865: PRO62927 Figure 832: DNA324149, NM_000993, Figure 866: DNA324168, XM_043173, gen.NM_000993 gen.XM_043173 Figure 833: PRO11197 Figure 867: DNA324169, XM_092489, Figure 834: DNA324150, NM_017546, gen.XM_092489 gen.NM_017546 Figure 868: PRO80868 Figure 835: PRO80850 Figure 869: DNA324170, XM_115672, Figure 836: DNA324151, NM_001450, gen.XM_115672 gen.NM_001450 Figure 870: PRO80869 Figure 837: PRO80851 Figure 871: DNA324171, NM_020548, Figure 838: DNA324152, XM_114229, gen.NM_020548 gen.XM_114229 Figure 872: PRO60753 Figure 839: DNA324153, XM_087122, Figure 873: DNA324172, XM_037101,

gen.XM_037101 Figure 910: DNA324190, XM_166007, Figure 874: PRO80870 gen.XM_166007 Figure 875: DNA324173, NM_032390, Figure 911: DNA324191, XM_015922, gen.NM_032390 gen.XM_015922 Figure 876: PRO80871 Figure 912: DNA324192, XM_087061, Figure 877: DNA324174, XM _002447, gen.XM_087061 gen.XM_002447 Figure 913: PRO80888 Figure 878: DNA324175, NM_033416. Figure 914: DNA324193, XM_087062, gen.NM_033416 gen.XM_087062 Figure 879: PRO80873 Figure 915: PRO80889 Figure 880: DNA324176, XM_016288. Figure 916: DNA324194, NM_001463, gen.XM_016288 gen.NM_001463 Figure 881: DNA272127, NM _003937, Figure 917: PRO80890 gen.NM_003937 Figure 918: DNA324195, XM_092158, Figure 882: PRO60397 gen.XM_092158 Figure 883: DNA324177, XM_030582, Figure 919: PRO80891 gen.XM_030582 Figure 920: DNA324196, XM_059351, Figure 884: PRO80875 gen.XM_059351 Figure 885: DNA324178, NM_015702, Figure 921A-B: DNA324197, NM_000090. gen.NM_015702 gen.NM_000090 Figure 886: PRO80876 Figure 922: PRO2665 Figure 887: DNA324179, NM_016838, Figure 923: DNA324198, NM_014585. gen.NM_016838 gen.NM_014585 Figure 888: PRO80877 Figure 924: PRO37675 Figure 889: DNA324180, NM_016839, Figure 925: DNA324199, XM_010778, gen.NM_016839 gen.XM_010778 Figure 890: PRO80878 Figure 926: DNA324200, XM_086961, Figure 891: DNA324181, XM_087118, gen.XM_086961 gen.XM_087118 Figure 927: DNA324201, XM_165994, Figure 892: PRO80879 gen.XM_165994 Figure 893: DNA324182, XM_165998, Figure 928: DNA324202, XM_045170, gen.XM_165998 gen.XM_045170 Figure 894: DNA324183, NM_001935, Figure 929: DNA324203, XM_113390, gen.NM_001935 gen.XM_113390 Figure 895: PRO80881 Figure 930: DNA299899, NM_002157. Figure 896: DNA324184, NM_020675, gen.NM_002157 gen.NM_020675 Figure 931: PRO62760 Figure 897: PRO80882 -Figure 932: DNA324204, XM_087045, Figure 898: DNA88051, NM_000079, gen.NM_000079 gen.XM_087045 Figure 899: PRO2146 Figure 933: DNA324205, XM_086944, Figure 900: DNA324185, XM_166008, gen.XM_086944 gen.XM_166008 Figure 934: DNA271608, NM_014670, Figure 901: DNA324186, XM_087240, gen.NM_014670 gen.XM_087240 Figure 935: PRO59895 Figure 902: PRO11403 Figure 936: DNA324206, XM_027963, Figure 903: DNA324187, NM_013341, gen.XM_027963 gen.NM_013341 Figure 937: PRO80900 Figure 904: PRO80883 Figure 938: DNA324207, XM_010852, Figure 905: DNA304805, NM_031942, gen.XM_010852 gen.NM_031942 Figure 939: PRO80901 Figure 906: PRO69531 Figure 940: DNA324208, XM_028034, Figure 907: DNA324188, XM_059465, gen.XM_028034 gen.XM_059465 Figure 941: DNA324209, NM_015934, Figure 908: PRO80884 gen.NM_015934 Figure 909: DNA324189, XM_015920, Figure 942: DNA324210, XM_087028, gen.XM_015920 gen.XM_087028

Figure 943: PRO80903 Figure 979: DNA324230, XM_050638. Figure 944: DNA324211, XM_092346, gen.XM_050638 gen.XM_092346 Figure 980A-B: DNA324231, NM_002846, Figure 945: PRO80904 gen.NM_002846 Figure 946: DNA324212, XM_002669, Figure 981: PRO2610 gen.XM_002669 Figure 982: DNA324232, NM_006000, Figure 947: PRO80905 gen.NM_006000 Figure 948: DNA324213, NM_021121, Figure 983: PRO26228 gen.NM_021121 Figure 984: DNA324233, XM_050891, Figure 949: PRO23124 gen.XM_050891 Figure 950: DNA324214, NM_001959, Figure 985: DNA324234, XM_087162, gen.NM_001959 gen.XM_087162 Figure 951: PRO23124 Figure 986: DNA324235, XM_058098, Figure 952: DNA324215, XM_030834, gen.XM_058098 gen.XM_030834 Figure 987: PRO80920 Figure 953: PRO80906 Figure 988: DNA324236, NM_022453, Figure 954A-C: DNA324216, XM_055254, gen.NM_022453 gen.XM_055254 Figure 989: PRO80921 Figure 955: DNA324217, NM_004044, Figure 990: DNA324237, NM_032726, gen.NM_004044 gen.NM_032726 Figure 956: PRO80908 Figure 991: PRO70675 Figure 957: DNA324218, XM_114298, Figure 992: DNA324238, XM_010866, gen.XM_114298 gen.XM_010866 Figure 958: DNA324219, NM_021141, Figure 993: DNA324239, XM_087166, gen.NM_021141 gen.XM_087166 Figure 959: PRO59313 Figure 994: DNA254204, NM_001087, Figure 960A-B: DNA324220, XM_098048, gen.NM_001087 gen.XM_098048 Figure 995: PRO49316 Figure 961: PRO80910 Figure 996: DNA324240, NM_005731, Figure 962: DNA324221, XM_098047, gen.NM_005731 gen.XM_098047 Figure 997: PRO80924 Figure 963: PRO80911 Figure 998: DNA189697, NM_004846, Figure 964: DNA324222, XM_002636, gen.NM_004846 gen.XM_002636 Figure 999: PRO23123 Figure 965: DNA324223, XM_087181, Figure 1000: DNA324241, NM_025202, gen.XM_087181 gen.NM_025202 Figure 966: DNA324224, NM_000998, Figure 1001: PRO80925 gen.NM_000998 Figure 1002: DNA324242, XM_115825, Figure 967: PRO10498 gen.XM_115825 Figure 968: DNA324225, XM_059422, Figure 1003: PRO80926 gen.XM_059422 Figure 1004: DNA324243, XM_010858, Figure 969: PRO9984 gen.XM_010858 Figure 970: DNA324226, XM_092545, Figure 1005: PRO80927 gen.XM_092545 Figure 1006: DNA324244, XM_002540, Figure 971: DNA324227, XM_059461, gen.XM_002540 gen.XM_059461 Figure 1007: DNA324245, XM_048690, Figure 972: PRO80915 gen.XM_048690 Figure 973: DNA324228, NM_018674, Figure 1008: PRO80929 gen.NM_018674 Figure 1009: DNA324246, NM_030926, Figure 974: PRO80916 gen.NM_030926 Figure 975: DNA324229, XM_050962, Figure 1010: PRO80930 gen.XM_050962 Figure 1011: DNA324247, XM_087218, Figure 976: PRO80917 gen.XM_087218 Figure 977: DNA 194827, NM_012100, Figure 1012: DNA324248, NM_004509,

gen.NM_004509

Figure 1013: PRO80932

gen.NM_012100

Figure 978: PRO24091

Figure 1014: DNA324249, NM_004510, Figure 1049: DNA324269, NM_006354, gen.NM_004510 gen.NM_006354 Figure 1050: PRO80952 Figure 1015: PRO80933 Figure 1051: DNA324270, NM_133480, Figure 1016: DNA324250, NM_080424, gen.NM_080424 gen.NM_133480 Figure 1052: PRO80953 Figure 1017: PRO80934 Figure 1053: DNA324271, NM_133481, Figure 1018: DNA324251, NM_018410, gen.NM_133481 gen.NM_018410 Figure 1019: PRO80935 Figure 1054: PRO80954 Figure 1055: DNA324272, NM_005718, Figure 1020: DNA324252, NM _017974, gen.NM_005718 gen.NM_017974 Figure 1021: PRO80936 Figure 1056: PRO80955 Figure 1057: DNA324273, NM_015644, Figure 1022A-B: DNA324253, XM_096169, gen.NM_015644 gen.XM_096169 Figure 1023: PRO80937 Figure 1058: PRO80956 Figure 1024: DNA150884, NM_005855, Figure 1059: DNA324274, XM_059561, gen.XM_059561 gen.NM_005855 Figure 1060: DNA324275, XM_052310, Figure 1025: PRO12520 gen.XM_052310 Figure 1026A-B: DNA324254, NM_004735, Figure 1061: PRO80958 gen.NM_004735 Figure 1062: DNA269910, NM _006395, Figure 1027: PRO80938 gen.NM_006395 Figure 1028A-C: DNA324255, XM_030203, gen.XM_030203 Figure 1063: PRO58308 Figure 1064: DNA324276, NM_000994, Figure 1029: DNA324256, XM _059372, gen.NM_000994 gen.XM_059372 Figure 1065: PRO80959 Figure 1030: DNA324257, NM .002712, gen.NM_002712 Figure 1066: DNA151017, NM_004844, gen.NM_004844 Figure 1031: PRO80941 Figure 1067: PRO12841 Figure 1032A-B: DNA324258, XM_042326, Figure 1068: DNA324277, XM_059557, gen.XM_042326 gen.XM_059557 Figure 1033: PRO80942 Figure 1069: PRO80960 Figure 1034: DNA324259, NM_004404, Figure 1070A-B: DNA324278, XM_042860, gen.NM_004404 gen.XM_042860 Figure 1035: PRO80943 Figure 1071: PRO80961 Figure 1036: DNA324260, XM_002742, Figure 1072: DNA324279, XM_042841, gen.XM_002742 Figure 1037: DNA324261, NM_138483, gen.XM_042841 gen.NM_138483 Figure 1073: PRO80962 Figure 1038: PRO80945 Figure 1074: DNA324280, XM_053712, Figure 1039: DNA324262, XM_115706, gen.XM_053712 gen.XM_115706 Figure 1075: DNA324281, XM_087284, gen.XM_087284 Figure 1040: DNA324263, XM_115722, Figure 1076: DNA324282, NM_002948, gen.XM_115722 Figure 1041: DNA324264, XM_084141, gen.NM_002948 Figure 1077: PRO6360 gen.XM_084141 Figure 1078: DNA324283, XM_053323, Figure 1042: DNA324265, XM_005086, gen.XM_053323 gen.XM_005086 Figure 1079A-B: DNA324284, NM_001068, Figure 1043: DNA324266, NM_015453, gen.NM_015453 gen.NM_001068 Figure 1080: PRO80966 Figure 1044: PRO80949 Figure 1081: DNA252367, NM_017801, Figure 1045: DNA324267, NM_022485, gen.NM_022485 gen.NM_017801 Figure 1046: PRO80950 Figure 1082: PRO48357 Figure 1083: DNA324285, XM_093624, Figure 1047A-B: DNA324268, XM_054520, gen.XM_093624 gen.XM_054520

Figure 1084: PRO80967

Figure 1048: PRO80951

Figure 1085: DNA324286, XM_046401, gen.XM_087588 gen.XM_046401 Figure 1121: DNA324302, XM_166011. Figure 1086: DNA324287, NM_022461, gen.XM_166011 gen.NM_022461 Figure 1122A-B: DNA324303, XM_114364, Figure 1087: PRO80969 gen.XM_114364 Figure 1088: DNA324288, XM_113410, Figure 1123A-B: DNA324304, XM_033294, gen.XM_113410 gen.XM_033294 Figure 1089: DNA88100, NM_000404, Figure 1124: PRO80983 gen.NM_000404 Figure 1125: DNA324305, NM_138614, Figure 1090: PRO2172 gen.NM_138614 Figure 1091: DNA324289, XM_091076, Figure 1126: PRO80984 gen.XM_091076 Figure 1127: DNA324306, XM_002899, Figure 1092: PRO80970 gen.XM_002899 Figure 1093A-B: DNA271187, NM_005109, Figure 1128: DNA225910, NM_004345, gen.NM_005109 gen.NM_004345 Figure 1094: PRO59504 Figure 1129: PRO36373 Figure 1095: DNA324290, NM_002468, Figure 1130: DNA324307, XM_010953, gen.NM_002468 gen.XM_010953 Figure 1096: PRO36735 Figure 1131: DNA324308, XM_051518, Figure 1097: DNA269930, NM_001607, gen.XM_051518 gen.NM_001607 Figure 1132A-D: DNA324309, NM_001407, Figure 1098: PRO58328 gen.NM_001407 Figure 1099: DNA270401, NM_003149, Figure 1133: PRO50095 gen.NM_003149 Figure 1134: DNA324310, NM_003365, Figure 1100: PRO58784 gen.NM_003365 Figure 1101: DNA324291, XM_087370, Figure 1135: PRO80988 gen.XM_087370 Figure 1136: DNA324311, XM_003245, Figure 1102: PRO80971 gen.XM_003245 Figure 1103: DNA324292, XM_098158, Figure 1137: DNA324312, XM_047561, gen.XM_098158 gen.XM_047561 Figure 1104: PRO80972 Figure 1138: PRO80990 Figure 1105: DNA324293, XM_017364, Figure 1139: DNA324313, XM_116853, gen.XM_017364 gen.XM_116853 Figure 1106: DNA324294, XM_087349, Figure 1140A-B: DNA324314, XM_113405, gen.XM_087349 gen.XM_113405 Figure 1107: PRO80974 Figure 1141: DNA324315, XM_114323, Figure 1108: DNA226547, NM_002295, gen.XM_114323 gen.NM_002295 Figure 1142: PRO80993 Figure 1109: PRO37010 Figure 1143: DNA324316, XM_002828, Figure 1110: DNA324295, NM_003973, gen.XM_002828 gen.NM_003973 Figure 1144: PRO80994 Figure 1111: PRO80975 Figure 1145: DNA150976, NM_022171, Figure 1112: DNA324296, XM_030417, gen.NM_022171 gen.XM_030417 Figure 1146: PRO12565 Figure 1113: DNA324297, NM_020347, Figure 1147: DNA324317, XM_041507, gen.NM_020347 gen.XM_041507 Figure 1114: PRO80977 Figure 1148: PRO71103 Figure 1115: DNA324298, XM_087346. Figure 1149: DNA103505, NM_004636, gen.XM_087346 gen.NM_004636 Figure 1116: PRO80978 Figure 1150: PRO4832 Figure 1117: DNA324299, XM_096198, Figure 1151: DNA324318, NM_006764, gen.XM_096198 gen.NM_006764 Figure 1118: PRO80979 Figure 1152: PRO80995 Figure 1119: DNA324300, XM_003222, Figure 1153: DNA150562, NM_007275, gen.XM_003222 gen.NM_007275 Figure 1120: DNA324301, XM_087588, Figure 1154: PRO12779

Figure 1155: DNA254582, NM_004635, Figure 1191: PRO81010 gen.NM_004635 Figure 1192: DNA324336, XM_166015, Figure 1156: PRO49685 gen.XM_166015 Figure 1157: DNA324319, NM_052859, Figure 1193: DNA324337, XM_113395, gen.NM_052859 gen.XM_113395 Figure 1158: PRO80996 Figure 1194: PRO81012 Figure 1159: DNA324320, NM_001064, Figure 1195: DNA269730, NM_014814, gen.NM_001064 gen.NM_014814 Figure 1160: PRO80997 Figure 1196: PRO58140 Figure 1161: DNA324321, XM_041211, Figure 1197: DNA324338, XM_036938. gen.XM_041211 gen.XM_036938 Figure 1162: DNA324322, XM_003213, Figure 1198: DNA324339, XM_029369, gen.XM_003213 gen.XM_029369 Figure 1163A-C: DNA324323, XM_037423, Figure 1199: DNA324340, XM_076414, gen.XM_037423 gen.XM_076414 Figure 1164: PRO80999 Figure 1200: PRO81015 Figure 1165A-B: DNA227307, NM_007184, Figure 1201: DNA324341, XM_093546, gen.NM_007184 gen.XM_093546 Figure 1166: PRO37770 Figure 1202: DNA324342, XM_113409, Figure 1167: DNA324324, NM_000688, gen.XM_113409 gen.NM_000688 Figure 1203: DNA324343, XM_087268, Figure 1168: PRO81000 gen.XM_087268 Figure 1169: DNA324325, XM_067715, Figure 1204: DNA324344, XM_116071, gen.XM_067715 gen.XM_116071 Figure 1170: DNA324326, NM_000992, Figure 1205: DNA324345, XM_116072, gen.NM_000992 gen.XM_116072 Figure 1171: PRO62153 Figure 1206: DNA324346, NM_000986, Figure 1172: DNA324327, NM_000666, gen.NM_000986 gen.NM_000666 Figure 1207: PRO10602 Figure 1173: PRO81002 Figure 1208: DNA324347, XM_015462, Figure 1174: DNA324328, NM_032750, gen.XM_015462 Figure 1209: DNA324348, XM_167366, gen.NM_032750 Figure 1175: PRO81003 gen.XM_167366 Figure 1176: DNA324329, NM_033008, Figure 1210: PRO81022 gen.NM_033008 Figure 1211: DNA324349, XM_087331, Figure 1177: PRO81004 gen.XM_087331 Figure 1178: DNA324330, NM_033010, Figure 1212: PRO81023 gen.NM_033010 Figure 1213: DNA324350, XM_039952, Figure 1179: PRO81005 gen.XM_039952 Figure 1180: DNA324331, NM_020418, Figure 1214: DNA324351, XM_045290, gen.NM_020418 gen.XM_045290 Figure 1181: PRO81006 Figure 1215: PRO81025 Figure 1182: DNA273919, NM_004704, Figure 1216A-B: DNA324352, NM_007085, gen.NM_004704 gen.NM_007085 Figure 1183: PRO61870 Figure 1217: PRO2077 Figure 1184A-B: DNA324332, XM_087448, Figure 1218: DNA324353, NM_004547, gen.XM_087448 gen.NM_004547 Figure 1185: PRO81007 Figure 1219: PRO81026 Figure 1220: DNA324354, XM_027161, Figure 1186: DNA324333, XM_002855, gen.XM_002855 gen.XM_027161 Figure 1187: DNA324334, XM_002854, Figure 1221A-B: DNA324355, XM_032269, gen.XM_002854 gen.XM_032269 Figure 1188: DNA0, NM_002854, gen.NM_002854 Figure 1222: PRO81028 Figure 1189: PRO Figure 1223: DNA88547, NM_006810, Figure 1190: DNA324335, XM_096195, gen.NM_006810 gen.XM_096195 Figure 1224: PRO2837

Figure 1225: DNA324356, XM_114301, Figure 1259: PRO81046 gen.XM_114301 Figure 1260: DNA324378, NM_000532, Figure 1226: PRO81029 gen.NM_000532 Figure 1227: DNA324357, XM_098173, Figure 1261: PRO81047 gen.XM_098173 Figure 1262: DNA324379, XM_036118, Figure 1228: PRO81030 gen.XM_036118 Figure 1229: DNA324358, XM_042618, Figure 1263: DNA324380, XM_084123, gen.XM_042618 gen.XM_084123 Figure 1230: PRO81031 Figure 1264: DNA324381, XM_018149, Figure 1231: DNA324359, XM_084129, gen.XM_018149 gen.XM_084129 Figure 1265: DNA324382, XM_087342. Figure 1232: DNA324360, XM_098154, gen.XM_087342 gen.XM_098154 Figure 1266: DNA324383, XM_059516, Figure 1233: PRO81033 gen.XM_059516 Figure 1234: DNA324361, XM_050552, Figure 1267: DNA324384, XM_087341, gen.XM_050552 gen.XM_087341 Figure 1235: DNA324362, NM_032343, Figure 1268: DNA324385, XM_165451. gen.NM_032343 gen.XM_165451 Figure 1236: PRO81034 Figure 1269: PRO81053 Figure 1237: DNA324363, XM_051264, Figure 1270: DNA269858, NM_004766. gen.XM_051264 gen.NM_004766 Figure 1238A-B: DNA324364, NM_013336, Figure 1271: PRO58259 gen.NM_013336 Figure 1272: DNA324386, NM_030921, Figure 1239: PRO1314 gen.NM_030921 Figure 1240: DNA324365, XM_067264, Figure 1273: PRO51109 gen.XM_067264 Figure 1274: DNA324387, XM_002859, Figure 1241: PRO81036 gen.XM_002859 Figure 1242: DNA324366, XM_114309, Figure 1275: DNA324388, XM_166014, gen.XM_114309 gen.XM_166014 Figure 1243: DNA324367, XM_084111, Figure 1276: DNA324389, NM_013363, gen.XM_084111 gen.NM_013363 Figure 1244: DNA324368, XM_113397, Figure 1277: PRO287 gen.XM_113397 Figure 1278: DNA324390, XM_058267, Figure 1245: DNA324369, XM_098111, gen.XM_058267 gen.XM_098111 Figure 1279: PRO81056 Figure 1246: DNA324370, NM_004637. Figure 1280A-B: DNA324391, NM_032383, gen.NM_004637 gen.NM_032383 Figure 1247: PRO81040 Figure 1281: PRO81057 Figure 1248: DNA324371, NM_020701, Figure 1282: DNA324392, NM_015472, gen.NM_020701 gen.NM_015472 Figure 1249: PRO81041 Figure 1283: PRO81058 Figure 1250: DNA324372, NM_003418, Figure 1284: DNA324393, NM_014445, gen.NM_003418 gen.NM_014445 Figure 1251: PRO81042 Figure 1285: PRO11048 Figure 1252: DNA324373, XM_059583, Figure 1286: DNA324394, XM_042168, gen.XM_059583 gen.XM_042168 Figure 1253: PRO81043 Figure 1287: PRO81059 Figure 1254: DNA324374, XM_113417, Figure 1288A-B: DNA324395, XM_114356, gen.XM_113417 gen.XM_114356 Figure 1255: DNA324375, XM_093487, Figure 1289: DNA324396, XM_105236, gen.XM_093487 gen.XM_105236 Figure 1256A-B: DNA324376, XM_030812, Figure 1290: DNA324397, XM_010978, gen.XM_030812 gen.XM_010978 Figure 1257: PRO58177 Figure 1291: DNA324398, XM_017356. Figure 1258A-B: DNA324377, XM_039805, gen.XM_017356 gen.XM_039805 Figure 1292A-B: DNA324399, XM_039796,

gen.XM_039796 Figure 1327: DNA89239, NM _000893, Figure 1293: PRO81064 gen.NM_000893 Figure 1294: DNA324400, XM_016334, Figure 1328: PRO2906 gen.XM_016334 Figure 1329: DNA324420, XM_113422, Figure 1295: DNA324401, XM_116058. gen.XM_113422 gen.XM_116058 Figure 1330: DNA225592, NM_001622, Figure 1296: DNA324402, XM_113408, gen.NM_001622 gen.XM_113408 Figure 1331: PRO36055 Figure 1297: DNA324403, NM_002492, Figure 1332: DNA324421, XM_005180, gen.NM_002492 gen.XM_005180 Figure 1298: PRO81068 Figure 1333: DNA324422, XM_087392, Figure 1299: DNA324404, XM_037381, gen.XM_087392 gen.XM_037381 Figure 1334: PRO81086 Figure 1300: DNA324405, XM_037377. Figure 1335A-B: DNA272605, NM_003722, gen.XM_037377 gen.NM_003722 Figure 1301: PRO69681 Figure 1336: PRO60741 Figure 1302A-B: DNA324406, XM_087254, Figure 1337: DNA324423, XM_117311, gen.XM_087254 gen.XM_117311 Figure 1303: PRO81070 Figure 1338: DNA324424, XM_116034, Figure 1304: DNA324407, XM_037600, gen.XM_116034 gen.XM_037600 Figure 1339: PRO81088 Figure 1305: PRO81071 Figure 1340A-B: DNA324425, XM_084110, Figure 1306: DNA324408, NM_018023, gen.XM_084110 gen.NM_018023 Figure 1341: DNA324426, XM_038243, Figure 1307: PRO81072 gen.XM_038243 Figure 1308: DNA324409, XM_093423, Figure 1342: PRO81090 gen.XM_093423 Figure 1343: DNA324427, XM_087359, Figure 1309: PRO81073 gen.XM_087359 Figure 1310: DNA324410, XM_029136, Figure 1344: DNA324428, XM_114328. gen.XM_029136 gen.XM_114328 Figure 1311: PRO81074 Figure 1345: DNA324429, XM_098109, Figure 1312: DNA324411, XM_087322, gen.XM_098109 gen.XM_087322 Figure 1346: PRO81093 Figure 1313A-B: DNA324412, XM_029132, Figure 1347: DNA324430, XM_087410, gen.XM_029132 gen.XM_087410 Figure 1314A-B: DNA324413, XM_029104, Figure 1348: DNA324431, NM_033316, gen.XM_029104 gen.NM_033316 Figure 1315: DNA324414, XM_084120, Figure 1349: PRO81095 gen.XM_084120 Figure 1350: DNA324432, XM_166017, Figure 1316: DNA254620, NM_005787. gen.XM_166017 gen.NM_005787 Figure 1351: PRO81096 Figure 1317: PRO49722 Figure 1352: DNA79129, NM_001647, Figure 1318: DNA324415, NM_032331, gen.NM_001647 gen.NM_032331 Figure 1353: PRO2551 Figure 1319: PRO81079 Figure 1354: DNA324433, NM_032288, Figure 1320: DNA324416, XM_011074, gen.NM_032288 gen.XM_011074 Figure 1355: PRO81097 Figure 1321: PRO81080 Figure 1356: DNA324434, XM_086228, Figure 1322: DNA324417, XM_087295, gen.XM_086228 gen.XM_087295 Figure 1357: PRO81098 Figure 1323: DNA324418, XM_087289, Figure 1358: DNA324435, XM_087278, gen.XM_087289 gen.XM_087278 Figure 1324: PRO81082 Figure 1359: DNA324436, XM_018523, Figure 1325: DNA324419, XM_105658, gen.XM_018523 gen.XM_105658 Figure 1360: DNA324437, XM_087297, Figure 1326: PRO81083 gen.XM_087297

Figure 1361: DNA324438, XM_002255, Figure 1397: PRO60542 gen.XM_002255 Figure 1398A-B: DNA324455, XM_052626, Figure 1362: PRO81102 gen.XM_052626 Figure 1363: DNA324439, XM_053122, Figure 1399: PRO81118 gen.XM_053122 Figure 1400: DNA324456, NM_016930, Figure 1364: DNA324440, XM_042695, gen.NM_016930 gen.XM_042695 Figure 1401: PRO81119 Figure 1365: DNA324441, XM_011160, Figure 1402: DNA324457, XM_035824, gen.XM_011160 gen.XM_035824 Figure 1366: DNA324442, NM_007100, Figure 1403: PRO81120 gen.NM_007100 Figure 1404: DNA324458, NM _033296, Figure 1367: PRO81106 gen.NM_033296 Figure 1368: DNA139747, NM_002477. Figure 1405: PRO81121 gen.NM_002477 Figure 1406: DNA324459, NM_138699, Figure 1369: PRO9785 gen.NM_138699 Figure 1370: DNA253804, NM_032219. Figure 1407: PRO81122 gen.NM_032219 Figure 1408: DNA324460, XM_116285, Figure 1371: PRO49209 gen.XM_116285 Figure 1372: DNA324443, NM_138385, Figure 1409: PRO81123 gen.NM_138385 Figure 1410: DNA324461, XM_041221. Figure 1373: PRO81107 gen.XM_041221 Figure 1374: DNA324444, NM_006342, Figure 1411: PRO81124 gen.NM_006342 Figure 1412: DNA324462, XM_117351, Figure 1375: PRO81108 gen.XM_117351 Figure 1376A-C: DNA324445, NM_133330, Figure 1413: DNA324463, XM_039165, gen.NM_133330 gen.XM_039165 Figure 1377: PRO81109 Figure 1414: DNA324464, NM_025205, Figure 1378A-C: DNA324446, NM_014919, gen.NM_025205 gen.NM_014919 Figure 1415: PRO81127 Figure 1379: PRO81110 Figure 1416: DNA324465, XM_039173, Figure 1380A-C: DNA324447, NM_133332, gen.XM_039173 gen.NM_133332 Figure 1417: DNA324466, XM_039176, Figure 1381: PRO81111 gen.XM_039176 Figure 1382: DNA324448, NM _005663, Figure 1418: DNA324467, XM_087583, gen.NM_005663 gen.XM_087583 Figure 1383: PRO81112 Figure 1419: DNA324468, NM_017491. Figure 1384A-B: DNA324449, XM_098248, gen.NM_017491 gen.XM_098248 Figure 1420: PRO12077 Figure 1385: PRO81113 Figure 1421: DNA324469, NM_005112, Figure 1386: DNA270615, NM_002938, gen.NM_005112 gen.NM_002938 Figure 1422: PRO81131 Figure 1387: PRO58986 Figure 1423: DNA324470, XM_011129, Figure 1388A-B: DNA324450, NM_014190, gen.XM_011129 gen.NM_014190 Figure 1424A-B: DNA324471, XM_052530, Figure 1389: PRO81114 gen.XM_052530 Figure 1390A-B: DNA324451, NM_014189, Figure 1425: DNA324472, NM_000661, gen.NM_014189 gen.NM_000661 Figure 1391: PRO81115 Figure 1426: PRO81134 Figure 1392: DNA324452, XM_035572. Figure 1427A-B: DNA324473, NM_002913, gen.XM_035572 gen.NM_002913 Figure 1393: PRO81116 Figure 1428: PRO81135 Figure 1394A-B: DNA324453, NM_014556, Figure 1429A-B: DNA324474, XM_047477, gen.NM_014556 gen.XM_047477 Figure 1395: PRO81117 Figure 1430: DNA324475, NM_004181, Figure 1396: DNA324454, NM_001313, gen.NM_004181 gen.NM_001313 Figure 1431: PRO81137

Figure 1432: DNA324476, XM_003435, gen.XM_096203 gen.XM_003435 Figure 1465: DNA324498, XM_084158, Figure 1433: DNA324478, XM_010941. gen.XM_084158 gen.XM_010941 Figure 1466: DNA324499, XM_034710, Figure 1434: DNA324479, XM_059593, gen.XM_034710 gen.XM_059593 Figure 1467: PRO81156 Figure 1435: DNA324480, NM_001553, Figure 1468: DNA324500, XM_034713, gen.NM _001553 gen.XM_034713 Figure 1436: PRO81141 Figure 1469: DNA324501, XM_059633, Figure 1437: DNA257511, NM_032313, gen.XM_059633 gen.NM_032313 Figure 1470: DNA324502, XM_114426, Figure 1438: PRO52083 gen.XM_114426 Figure 1439: DNA324481, XM_071623, Figure 1471: DNA324503, XM_056957, gen.XM_071623 gen.XM_056957 Figure 1440A-B: DNA324482, XM_036002, Figure 1472: DNA324504, XM_088472, gen.XM_036002 gen.XM_088472 Figure 1441: DNA324483, XM_058927, Figure 1473: DNA324505, XM_114424, gen.XM_058927 gen.XM_114424 Figure 1442: DNA324484, XM_059628, Figure 1474A-B: DNA324506, XM_042301. gen.XM_059628 gen.XM_042301 Figure 1443: DNA324485, XM_046057, Figure 1475: PRO81163 gen.XM_046057 Figure 1476: DNA324507, XM_017925, Figure 1444: PRO81146 gen.XM_017925 Figure 1445: DNA324486, XM_031320, Figure 1477: DNA324508, XM_052336, gen.XM_031320 gen.XM_052336 Figure 1446: DNA225919, NM_001134, Figure 1478: DNA324509, NM_002106, gen.NM_001134 gen.NM_002106 Figure 1447: PRO36382 Figure 1479: PRO10297 Figure 1480: DNA324510, XM_085068, Figure 1448A-B: DNA324487, XM_003511. gen.XM_003511 gen.XM_085068 Figure 1449: DNA324488, NM _006835, Figure 1481: PRO81166 gen.NM_006835 Figure 1482: DNA324511, XM_165473, Figure 1450: PRO4605 gen.XM_165473 Figure 1451: DNA324489, XM_003305, Figure 1483: DNA324512, XM_087514, gen.XM_003305 gen.XM_087514 Figure 1452: DNA324490, XM_113425, Figure 1484: DNA324513, XM_116247, gen.XM_113425 gen.XM_116247 Figure 1453: DNA324491, XM_001389, Figure 1485: DNA324514, NM_002358, gen.XM_001389 gen.NM_002358 Figure 1486: PRO81169 Figure 1454: PRO81148 Figure 1455: DNA324492, XM_087527, Figure 1487: DNA324515, XM_050200, gen.XM_087527 gen.XM_050200 Figure 1488: PRO81170 Figure 1456: DNA324493, XM_035986, gen.XM_035986 Figure 1489: DNA225584, NM_001154, Figure 1457A-B: DNA324494, NM_014933, gen.NM_001154 gen.NM_014933 Figure 1490: PRO36047 Figure 1491: DNA324516, NM_024900, Figure 1458: PRO81150 Figure 1459: DNA290585, NM_000582, gen.NM_024900 gen.NM_000582 Figure 1492: PRO81171 Figure 1460: PRO70536 Figure 1493: DNA324517, XM_040752, Figure 1461: DNA324495, XM _055551, gen.XM_040752 gen.XM_055551 Figure 1494: DNA324518, NM_002413, Figure 1462: PRO81151 gen.NM_002413 Figure 1463: DNA324496, XM_087498, Figure 1495: PRO60956 Figure 1496: DNA324519, XM_114401, gen.XM_087498 Figure 1464: DNA324497, XM_096203, gen.XM_114401

Figure 1497: DNA324520, XM_068164, Figure 1532: DNA324538, XM_116204, gen.XM_068164 gen.XM_116204 Figure 1498: PRO81174 Figure 1533: DNA324539, XM_116205, Figure 1499: DNA324521, XM_060067, gen.XM_116205 gen.XM_060067 Figure 1534: DNA324540, XM_098405, Figure 1500: DNA324522, XM_003555, gen.XM_098405 gen.XM_003555 Figure 1535: DNA324541, XM_052313, Figure 1501: PRO81176 gen.XM_052313 Figure 1502: DNA324523, XM_034321, Figure 1536: PRO81195 gen.XM_034321 Figure 1537: DNA324542, XM_087659, Figure 1503: PRO81177 gen.XM_087659 Figure 1504: DNA324524, NM_006439. Figure 1538: PRO81196 gen.NM_006439 Figure 1539: DNA324543, XM_029096, Figure 1505: PRO81178 gen.XM_029096 Figure 1506: DNA324525, NM_001006, Figure 1540: DNA324544, XM_003825. gen.NM_001006 gen.XM_003825 Figure 1507: PRO81179 Figure 1541: DNA324545, XM_057994, Figure 1508: DNA227575, NM_005141, gen.XM_057994 gen.NM_005141 Figure 1542: PRO81199 Figure 1509: PRO38038 Figure 1543: DNA324546, XM_087686, Figure 1510: DNA324526, XM_114368, gen.XM_087686 gen.XM_114368 Figure 1544: DNA324547, XM_017641, Figure 1511A-B: DNA225920, NM _000508, gen.XM_017641 gen.NM_000508 Figure 1545: DNA324548, NM_030782, Figure 1512: PRO36383 gen.NM_030782 Figure 1513: DNA324527, NM_021871, Figure 1546: PRO81202 gen.NM_021871 Figure 1547: DNA324549, XM_084168, Figure 1514: PRO81181 gen.XM_084168 Figure 1515: DNA225921, NM_000509, Figure 1548: DNA324550, XM_057492. gen.NM_000509 gen.XM_057492 Figure 1516: PRO36384 Figure 1549: DNA324551, XM_087597, Figure 1517: DNA324528, NM_021870, gen.XM_087597 gen.NM_021870 Figure 1550: DNA324552, XM_087601. Figure 1518: PRO81182 gen.XM_087601 Figure 1519: DNA324529, XM_059623, Figure 1551: DNA324554, XM_087599, gen.XM_059623 gen.XM_087599 Figure 1520: DNA324530, XM_106246, Figure 1552: DNA324555, XM_114435, gen.XM_106246 gen.XM_114435 Figure 1521: PRO81184 Figure 1553: DNA324556, XM_087600. Figure 1522: DNA324531, NM_002129, gen.XM_087600 gen.NM_002129 Figure 1554: DNA324557, XM_016170, Figure 1523: PRO81185 gen.XM_016170 Figure 1524: DNA324532, XM_040321, Figure 1555: DNA324558, XM_114434, gen.XM_040321 gen.XM_114434 Figure 1525: DNA324533, XM_015563, Figure 1556: DNA324559, XM_113452, gen.XM_015563 gen.XM_113452 Figure 1526: DNA324534, NM_024748, Figure 1557: DNA324560, XM_071580, gen.NM_024748 gen.XM_071580 Figure 1527: PRO81188 Figure 1558: PRO81213 Figure 1528: DNA324535, XM_165470, Figure 1559: DNA324561, XM_087713, gen.XM_165470 gen.XM_087713 Figure 1529: PRO81189 Figure 1560: PRO81214 Figure 1530A-E: DNA324536, XM_003477, Figure 1561: DNA324562, XM_094440, gen.XM_003477 gen.XM_094440 Figure 1531: DNA324537, XM_165465, Figure 1562: DNA324563, XM_106739, gen.XM_165465 gen.XM_106739

Figure 1563: PRO81216 Figure 1597: DNA324584, XM_087610, Figure 1564: DNA324564, XM_087614, gen.XM_087610 gen.XM_087614 Figure 1598: DNA288259, NM_031966. Figure 1565: DNA324565, XM_004009. gen.NM_031966 gen.XM_004009 Figure 1599: PRO4676 Figure 1566: PRO81219 Figure 1600: DNA324585, XM_042025, Figure 1567: DNA324566, XM_114437, gen.XM_042025 gen.XM_114437 Figure 1601: PRO81238 Figure 1568: DNA324567, XM_043771. Figure 1602: DNA324586, NM_005713, gen.XM_043771 gen.NM_005713 Figure 1569: PRO81221 Figure 1603: PRO81239 Figure 1570: DNA324568, NM _000997. Figure 1604: DNA324587, XM_059709, gen.NM_000997 gen.XM_059709 Figure 1571: PRO11077 Figure 1605: PRO81240 Figure 1572: DNA324569, XM_003869, Figure 1606: DNA324588, XM_116447, gen.XM_003869 gen.XM_116447 Figure 1573: DNA227173, NM_001465, Figure 1607: PRO81241 gen.NM_001465 Figure 1608: DNA324589, XM_037260, Figure 1574: PRO37636 gen.XM_037260 Figure 1575: DNA324570, NM_018034, Figure 1609: DNA324590, XM_098351, gen.NM_018034 gen.XM_098351 Figure 1576: PRO81223 Figure 1610: DNA324591, XM_098354, Figure 1577: DNA324571, NM_032637, gen.XM_098354 gen.NM_032637 Figure 1611: DNA324592, XM_098352. Figure 1578: PRO81224 gen.XM_098352 Figure 1579: DNA324572, NM_005983, Figure 1612: DNA324593, XM_166037, gen.NM_005983 gen.XM_166037 Figure 1580: PRO81225 Figure 1613: PRO81246 Figure 1581A-B: DNA324573, XM_003896, Figure 1614: DNA324594, XM_041694. gen.XM_003896 gen.XM_041694 Figure 1582: DNA287282, NM_002130, Figure 1615: DNA324595, XM_165488, gen.NM_002130 gen.XM_165488 Figure 1583: PRO69554 Figure 1616: PRO81248 Figure 1584: DNA324574, XM_114442, Figure 1617: DNA324596, XM_059669, gen.XM_114442 gen.XM_059669 Figure 1585: PRO81227 Figure 1618: PRO81249 Figure 1586: DNA324575, XM_114439, Figure 1619: DNA324597, XM_027964, gen.XM_114439 gen.XM_027964 Figure 1587: DNA324576, XM_114440, Figure 1620: PRO81250 gen.XM_114440 Figure 1621: DNA324598, XM_088020, Figure 1588A-B: DNA324577, XM_032902. gen.XM_088020 gen.XM_032902 Figure 1622: DNA324599, XM_117387, Figure 1589: PRO81230 gen.XM_117387 Figure 1590: DNA324578, XM_032895, Figure 1623: DNA324600, XM_114469, gen.XM_032895 gen.XM_114469 Figure 1591: DNA324579, XM_084179, Figure 1624: DNA324601, NM_001207, gen.XM_084179 gen.NM_001207 Figure 1592: DNA324580, XM_041712, Figure 1625: PRO22771 gen.XM_041712 Figure 1626A-B: DNA324602, XM_032553, Figure 1593: DNA324581, XM_116439, gen.XM_032553 gen.XM_116439 Figure 1627: DNA254147, NM_000521, Figure 1594: PRO81234 gen.NM_000521 Figure 1595: DNA324582, XM_087611, Figure 1628: PRO49262 gen.XM_087611 Figure 1629: DNA324603, NM_031482, Figure 1596: DNA324583, XM_059653, gen.NM_031482 gen.XM_059653 Figure 1630: PRO81254

Figure 1631: DNA324604, XM_087790, Figure 1666: DNA324622, XM_003830, gen.XM_087790 gen.XM_003830 Figure 1632: DNA324605, NM_001025, Figure 1667: PRO81269 gen.NM_001025 Figure 1668: DNA324623, XM_037002, Figure 1633: PRO10685 gen.XM_037002 Figure 1634: DNA324606, XM_098362, Figure 1669: DNA324624, XM_166026, gen.XM_098362 gen.XM_166026 Figure 1635: PRO81256 Figure 1670: DNA324625, XM_041059, Figure 1636: DNA324607, NM_003401, gen.XM_041059 gen.NM_003401 Figure 1671: DNA83020, NM_000358, Figure 1637: PRO70327 gen.NM_000358 Figure 1638: DNA290231, NM_022550, Figure 1672: PRO2561 gen.NM_022550 Figure 1673: DNA324626, NM_003687, Figure 1639: PRO70327 gen.NM_003687 Figure 1640: DNA324608, XM_017857, Figure 1674: PRO81272 gen.XM_017857 Figure 1675: DNA324627, XM_034862, Figure 1641: DNA324609, XM_117398, gen.XM_034862 gen.XM_117398 Figure 1676: PRO34544 Figure 1642A-B: DNA257253, NM_032280, Figure 1677: DNA103380, NM_003374, gen.NM_032280 gen.NM_003374 Figure 1643: PRO51851 Figure 1678: PRO4710 Figure 1644: DNA324610, XM_003771, Figure 1679: DNA324628, XM_017474, gen.XM_003771 gen.XM_017474 Figure 1645: PRO81259 Figure 1680: PRO63082 Figure 1646A-B: DNA269816, NM_002397, Figure 1681A-B: DNA324629, NM_014829, gen.NM_002397 gen.NM_014829 Figure 1647: PRO58219 Figure 1682: PRO81273 Figure 1648: DNA324611, XM_116427, Figure 1683A-B: DNA324630, XM_114482, gen.XM_116427 gen.XM_114482 Figure 1649: PRO81260 Figure 1684: PRO81274 Figure 1650: DNA324612, NM_004772, Figure 1685: DNA324631, NM_004893, gen.NM_004772 gen.NM_004893 Figure 1651: PRO81261 Figure 1686: PRO81275 Figure 1652: DNA324613, XM_016674, Figure 1687: DNA269809, NM_006805, gen.XM_016674 gen.NM_006805 Figure 1653: PRO81262 Figure 1688: PRO58213 Figure 1654: DNA324614, XM_113463, Figure 1689: DNA226872, NM_001964, gen.XM_113463 gen.NM_001964 Figure 1655: DNA324615, XM_034744, Figure 1690: PRO37335 gen.XM_034744 Figure 1691: DNA324632, XM_116307, Figure 1656: DNA324616, XM_087745, gen.XM_116307 gen.XM_087745 Figure 1692: PRO81276 Figure 1657: PRO81264 Figure 1693: DNA324633, NM_004134, Figure 1658: DNA324617, XM_018473, gen.NM_004134 gen.XM_018473 Figure 1694: PRO81277 Figure 1659: PRO81265 Figure 1695: DNA324634, XM_038221, Figure 1660: DNA324618, XM_087635, gen.XM_038221 gen.XM_087635 Figure 1696: PRO81278 Figure 1661: PRO81266 Figure 1697: DNA271931, NM_005754, Figure 1662: DNA324619, XM_087637, gen.NM_005754 gen.XM_087637 Figure 1698: PRO60207 Figure 1663: DNA324620, XM_166027, Figure 1699: DNA324635, XM_003841, gen.XM_166027 gen.XM_003841 Figure 1664: DNA324621, NM_014035, Figure 1700: DNA324636, XM_032759, gen.NM_014035 gen.XM_032759 Figure 1665: PRO1285 Figure 1701: DNA324637, XM_017591,

gen.XM_017591 gen.NM_018913 Figure 1702: DNA324638, NM_006058, Figure 1737: PRO81293 gen.NM_006058 Figure 1738A-B: DNA324656, NM_018914, Figure 1703: PRO81280 gen.NM_018914 Figure 1704: DNA324639, NM_002084, 1 Figure 1739: PRO81294 gen.NM_002084 Figure 1740A-B: DNA324657, NM_018915, Figure 1705: PRO81281 gen.NM_018915 Figure 1706: DNA324640, NM_018047, Figure 1741: PRO36020 gen.NM_018047 Figure 1742A-B: DNA324658, NM_018916. Figure 1707: PRO81282 gen.NM_018916 Figure 1708: DNA324641, NM_005617, Figure 1743: PRO81295 gen.NM_005617 Figure 1744A-B: DNA324659, NM_018917, Figure 1709: PRO10849 gen.NM_018917 Figure 1710: DNA324642, XM_003937, Figure 1745: PRO81296 gen.XM_003937 Figure 1746A-B: DNA324660, NM_018918, Figure 1711: DNA324643, XM_087621. gen.NM_018918 gen.XM_087621 Figure 1747: PRO81297 Figure 1712A-B: DNA324644, XM_003789, Figure 1748A-B: DNA324661, NM_018919, gen.XM_003789 gen.NM_018919 Figure 1713: DNA324645, XM_087652, Figure 1749: PRO81298 gen.XM_087652 Figure 1750A-B: DNA324662, NM_018920, Figure 1714: DNA324646, XM_068853. gen.NM_018920 gen.XM_068853 Figure 1751: PRO81299 Figure 1715: PRO81286 Figure 1752A-B: DNA324663, NM_018921, Figure 1716: DNA324647, XM_116465, gen.NM_018921 gen.XM_116465 Figure 1753: PRO81300 Figure 1717: PRO81287 Figure 1754A-B: DNA324664, NM_018922, Figure 1718: DNA302020, NM _005573, gen.NM_018922 gen.NM_005573 Figure 1755: PRO81301 Figure 1719: PRO70993 Figure 1756A-B: DNA324665, NM_018923, Figure 1720: DNA324648, XM_113467, gen.NM_018923 gen.XM_113467 Figure 1757: PRO81302 Figure 1721: DNA271626, NM_014773, Figure 1758A-B: DNA324666, NM_018924, gen.NM_014773 gen.NM_018924 Figure 1722: PRO59913 Figure 1759: PRO81303 Figure 1723A-B: DNA324649, XM_056315, Figure 1760A-B: DNA324667, NM_018925, gen.XM_056315 gen.NM_018925 Figure 1724: DNA324650, NM_024668, Figure 1761: PRO81304 gen.NM_024668 Figure 1762A-B: DNA324668, NM_018926, Figure 1725: PRO81289 gen.NM_018926 Figure 1726: DNA324651, NM_080670, Figure 1763: PRO81305 gen.NM_080670 Figure 1764A-B: DNA324669, NM_018927, Figure 1727: PRO81290 gen.NM_018927 Figure 1728A-B: DNA324652, NM_002588, Figure 1765: PRO37091 gen.NM_002588 Figure 1766A-B: DNA324670, NM_018928, Figure 1729: PRO81291 gen.NM_018928 Figure 1730A-B: DNA324653, NM_003735, Figure 1767: PRO81306 gen.NM_003735 Figure 1768A-B: DNA324671, NM_018929, Figure 1731: PRO81292 gen.NM_018929 Figure 1732A-B: DNA150679, NM_003736, Figure 1769: PRO81307 gen.NM_003736 Figure 1770A-B: DNA324672, NM_032088, Figure 1733: PRO12416 gen.NM_032088 Figure 1734A-B: DNA324654, NM_018912, Figure 1771: PRO81308 gen.NM_018912 Figure 1772A-B: DNA324673, NM_032092, Figure 1735: PRO36058 gen.NM_032092

Figure 1773: PRO81309

Figure 1736A-B: DNA324655, NM_018913,

Figure 1774: DNA324674, NM_032403, Figure 1809: PRO81327 gen.NM_032403 Figure 1810: DNA324694, XM_116856, Figure 1775: PRO81310 gen.XM_116856 Figure 1776: DNA324675, NM_032402, Figure 1811: DNA324695, XM_003716, gen.NM_032402 gen.XM_003716 Figure 1777: PRO81311 Figure 1812: DNA227320, NM _003714, Figure 1778: DNA324676, XM_098387, gen.NM_003714 gen.XM_098387 Figure 1813: PRO37783 Figure 1779: DNA324677, NM_002109, Figure 1814: DNA324696, NM_032361, gen.NM_002109 gen.NM_032361 Figure 1780: PRO4908 Figure 1815: PRO81330 Figure 1781: DNA324678, XM_084180, Figure 1816: DNA324697, XM_087773, gen.XM_084180 gen.XM_087773 Figure 1782: PRO81313 Figure 1817: DNA324698, XM_114457, Figure 1783: DNA324679, XM_039975, gen.XM_114457 gen.XM_039975 Figure 1818: DNA324699, XM_165483, Figure 1784: PRO81314 gen.XM_165483 Figure 1785: DNA324680, NM_033551, Figure 1819: DNA324700, XM_114453, gen.NM_033551 gen.XM_114453 Figure 1786: PRO81315 Figure 1820: DNA324701, XM_165484, Figure 1787: DNA324681, NM_004821, gen.XM_165484 gen.NM_004821 Figure 1821: DNA324702, XM_030771, Figure 1788: PRO81316 gen.XM_030771 Figure 1789: DNA324682, XM_068395, Figure 1822: PRO19615 gen.XM_068395 Figure 1823: DNA324703, XM_030777, Figure 1790: PRO81317 gen.XM_030777 Figure 1791: DNA226418, NM_004060, Figure 1824: DNA324704, XM_030782, gen.NM_004060 gen.XM_030782 Figure 1792: PRO36881 Figure 1825: PRO81336 Figure 1793A-B: DNA324683, XM_056963, Figure 1826: DNA324705, NM_030567, gen.XM_056963 gen.NM_030567 Figure 1794: PRO81318 Figure 1827: PRO81337 Figure 1795: DNA324684, NM_004219, Figure 1828: DNA225909, NM_000505, gen.NM_004219 gen.NM_000505 Figure 1796: PRO81319 Figure 1829: PRO36372 Figure 1797: DNA324685, XM_094243, Figure 1830: DNA274206, NM _006816, gen.XM_094243 gen.NM_006816 Figure 1798A-B: DNA324686, XM_047964, Figure 1831: PRO62135 gen.XM_047964 Figure 1832: DNA324706, NM_031300, Figure 1799: DNA324687, XM_016345, gen.NM_031300 gen.XM_016345 Figure 1833: PRO81338 Figure 1800: DNA324688, NM_002887, Figure 1834: DNA324707, NM_013237, gen.NM_002887 gen.NM_013237 Figure 1801: PRO81323 Figure 1835: PRO81339 Figure 1802: DNA324689, XM_166029, Figure 1836: DNA324708, NM_002011, gen.XM_166029 gen.NM_002011 Figure 1803: DNA324690, NM_002520, Figure 1837: PRO81340 gen.NM_002520 Figure 1838: DNA324709, NM_022963, Figure 1804: PRO58993 gen.NM_022963 Figure 1805: DNA324691, XM_043340, Figure 1839: PRO81341 gen.XM_043340 Figure 1840: DNA324710, XM_038946, Figure 1806: PRO81325 gen.XM_038946 Figure 1807: DNA324692, XM_116340, Figure 1841: DNA324711, XM_113454, gen.XM_116340 gen.XM_113454 Figure 1808A-B: DNA324693, XM_043388. Figure 1842: DNA324712, XM_166028, gen.XM_043388 gen.XM_166028

Figure 1843: DNA324713, NM_015043, Figure 1877: DNA324731, XM_168123, gen.NM_015043 gen.XM_168123 Figure 1844: PRO81345 Figure 1878: DNA324732, XM_166457, Figure 1845: DNA324714, XM_113468, gen.XM_166457 gen.XM_113468 Figure 1879: DNA324733, XM_166469, Figure 1846: DNA324715, NM_014275. gen.XM_166469 gen.NM_014275 Figure 1880: DNA324734, NM_018135, Figure 1847: PRO1927 gen.NM_018135 Figure 1848: DNA324716, NM_054013, Figure 1881: PRO81359 gen.NM_054013 Figure 1882A-B: DNA324735, XM_166340, Figure 1849: PRO81347 gen.XM_166340 Figure 1850: DNA270675, NM_005520, Figure 1883: DNA324736, XM_087960. gen.NM_005520 gen.XM_087960 Figure 1851: PRO59040 Figure 1884: DNA324737, XM_166362, Figure 1852: DNA324717, NM_006098. gen.XM_166362 gen.NM_006098 Figure 1885: PRO81362 Figure 1853: PRO25849 Figure 1886: DNA227204, NM_015388, Figure 1854: DNA269593, NM_005110, gen.NM_015388 gen.NM_005110 Figure 1887: PRO37667 Figure 1855: PRO58006 Figure 1888: DNA324738, XM_166425, Figure 1856: DNA324718, XM_116365, gen.XM_166425 gen.XM_116365 Figure 1889: PRO81363 Figure 1857: DNA324719, XM_116511. Figure 1890: DNA324739, NM_057161, gen.XM_116511 gen.NM_057161 Figure 1858: DNA324720, XM_087823, Figure 1891: PRO81364 gen.XM_087823 Figure 1892: DNA270613, NM_006245, Figure 1859A-C: DNA324721, XM_053955, gen.NM_006245 gen.XM_053955 Figure 1893: PRO58984 Figure 1860: DNA324722, XM_113476, Figure 1894: DNA324740, NM_006586, gen.XM_113476 gen.NM_006586 Figure 1861: DNA324723, XM_116514, Figure 1895: PRO81365 gen.XM_116514 Figure 1896: DNA324741, XM_166402, Figure 1862: DNA324724, XM_094741, gen.XM_166402 gen.XM_094741 Figure 1897: PRO81366 Figure 1863: DNA324725, NM_025168, Figure 1898: DNA324742, NM _001760, gen.NM_025168 gen.NM_001760 Figure 1864: PRO81354 Figure 1899: PRO81367 Figure 1865A-B: DNA324726, XM_165740, Figure 1900: DNA287246, NM_004053, gen.XM_165740 gen.NM_004053 Figure 1866: DNA272171, NM_002388, Figure 1901: PRO69521 gen.NM_002388 Figure 1902: DNA324743, NM_017601. Figure 1867: PRO60438 gen.NM_017601 Figure 1868: DNA324727, XM_167169, Figure 1903: PRO81368 gen.XM_167169 Figure 1904: DNA275630, NM_006708. Figure 1869: PRO81355 gen.NM_006708 Figure 1870: DNA324728, NM_014452, Figure 1905: PRO63253 gen.NM_014452 Figure 1906: DNA324744, NM_014341, Figure 1871: PRO868 gen.NM_014341 Figure 1872: DNA324729, XM_166349, Figure 1907: PRO81369 gen.XM_166349 Figure 1908: DNA304460, NM_016059, Figure 1873: PRO81356 gen.NM_016059 Figure 1874: DNA304680, NM_007355. Figure 1909: PRO4984 gen.NM_007355 Figure 1910: DNA324745, XM_166412, Figure 1875: PRO71106 gen.XM_166412 Figure 1876: DNA324730, XM_165772, Figure 1911: PRO81370 gen.XM_165772 Figure 1912: DNA304716, NM_078467.

gen.NM_078467 gen.NM_022551 Figure 1913: PRO71142 Figure 1947: PRO71088 Figure 1914: DNA324746, XM_166417, Figure 1948: DNA324767, XM_165747, gen.XM_166417 gen.XM_165747 Figure 1915: PRO81371 Figure 1949; DNA324768, XM_165698. Figure 1916A-B: DNA324747, NM_003137, gen.XM_165698 gen.NM_003137 Figure 1950: PRO4884 Figure 1917: PRO81372 Figure 1951A-B: DNA324769, XM_165770, Figure 1918A-B: DNA324748, NM_004117, gen.XM_165770 gen.NM_004117 Figure 1952: DNA287227, NM_004159. Figure 1919: PRO36841 gen.NM_004159 Figure 1920: DNA324749, XM_166419, Figure 1953: PRO69506 gen.XM_166419 Figure 1954: DNA324770, XM_165717, Figure 1921: DNA324750, XM_165794, gen.XM_165717 gen.XM_165794 Figure 1955: DNA324771, XM_166480. Figure 1922: DNA324751, NM_007104. gen.XM_166480 gen.NM_007104 Figure 1956: DNA324772, XM_165801, Figure 1923: PRO10360 gen.XM_165801 Figure 1924: DNA324752, NM_024294, Figure 1957A-B: DNA324773, NM_000592, gen.NM_024294 gen.NM_000592 Figure 1925: PRO81375 Figure 1958: PRO36316 Figure 1926: DNA324753, NM_022758, Figure 1959: DNA324774, NM _001710, gen.NM_022758 gen.NM_001710 Figure 1927: PRO50582 Figure 1960: PRO36305 Figure 1928: DNA324754, XM_168070, Figure 1961: DNA227607, NM _005346, gen.XM_168070 gen.NM_005346 Figure 1929: DNA324755, NM_012391, Figure 1962: PRO38070 gen.NM_012391 Figure 1963: DNA304668, NM_005345. Figure 1930: PRO81377 gen.NM_005345 Figure 1931: DNA324756, XM_166459, Figure 1964: PRO71095 gen.XM_166459 Figure 1965: DNA324775, NM_021177, Figure 1932: DNA324757, XM_166333, gen.NM_021177 gen.XM_166333 Figure 1966: PRO81394 Figure 1933: PRO81379 Figure 1967A-B: DNA272263, NM_006295, Figure 1934: DNA324758, XM_058039, gen.NM_006295 gen.XM_058039 Figure 1968: PRO70138 Figure 1935: PRO81380 Figure 1969: DNA287319, NM_001288. Figure 1936: DNA324759, XM_087990. gen.NM_001288 gen.XM_087990 Figure 1970: PRO69584 Figure 1937: DNA324760, XM_165743, Figure 1971: DNA324776, NM_001320, gen.XM_165743 gen.NM_001320 Figure 1938: DNA324761, XM_166360. Figure 1972: PRO63052 gen.XM_166360 Figure 1973A-B: DNA324777, NM_004639, Figure 1939: DNA324763, XM_059801, gen.NM_004639 gen.XM_059801 Figure 1974: PRO81395 Figure 1940: DNA324764, XM_166363. Figure 1975A-B: DNA324778, NM_080703, gen.XM_166363 gen.NM_080703 Figure 1941: DNA324765, XM_016857. Figure 1976: PRO81396 gen.XM_016857 Figure 1977A-B: DNA324779, NM_080702, Figure 1942: DNA227442, NM_001350, gen.NM_080702 gen.NM_001350 Figure 1978: PRO81397 Figure 1943: PRO37905 Figure 1979A-B: DNA324780, NM_004638, Figure 1944: DNA324766, NM_005452, gen.NM_004638 gen.NM_005452 Figure 1980: PRO81398 Figure 1945: PRO81387 Figure 1981A-B: DNA324781, NM_080686, Figure 1946: DNA304661, NM_022551. gen.NM_080686

Figure 1982: PRO81399 gen.NM_018950 Figure 1983: DNA324782, XM_165771, Figure 2018: PRO81414 gen.XM_165771 Figure 2019: DNA324800, XM_166392, Figure 1984: DNA324783, NM _080598. gen.XM_166392 gen.NM_080598 Figure 2020: PRO81415 Figure 1985: PRO71125 Figure 2021: DNA324801, XM_166336, Figure 1986: DNA304699, NM_004640, gen.XM_166336 gen.NM_004640 Figure 2022: PRO81416 Figure 1987: PRO71125 Figure 2023: DNA324802, XM_167128, Figure 1988: DNA324784, XM_165765, gen.XM_167128 gen.XM_165765 Figure 2024: PRO23797 Figure 1989: PRO81400 Figure 2025: DNA324803, XM_167161, Figure 1990: DNA324785, XM_087945, gen.XM_167161 gen.XM_087945 Figure 2026: PRO81417 Figure 1991: PRO81401 Figure 2027: DNA324804, NM_013375, Figure 1992: DNA324786, XM_166381, gen.NM_013375 gen.XM_166381 Figure 2028: PRO81418 Figure 1993: PRO81402 Figure 2029: DNA324805, NM_007047, Figure 1994: DNA324787, XM_168104, gen.NM_007047 gen.XM_168104 Figure 2030: PRO81419 Figure 1995: DNA324788, XM_166401, Figure 2031: DNA324806, XM_167179, gen.XM_166401 gen.XM_167179 Figure 1996: PRO81404 Figure 2032: DNA290785, NM_003107, Figure 1997: DNA271040, NM_001517, gen.NM_003107 gen.NM_001517 Figure 2033: PRO70544 Figure 1998: PRO59365 Figure 2034: DNA150772, NM _003472, Figure 1999A-B: DNA324789, XM_165738, gen.NM_003472 gen.XM_165738 Figure 2035: PRO12797 Figure 2000: DNA324790, XM_087939. Figure 2036A-B: DNA324807, XM_165728, gen.XM_087939 gen.XM_165728 Figure 2001: PRO81406 Figure 2037: DNA324808, XM_165749, Figure 2002: DNA324791, XM_166353, gen.XM_165749 gen.XM_166353 Figure 2038: PRO81421 Figure 2003: PRO1112 Figure 2039A-B: DNA324809, NM_004973, Figure 2004A-B: DNA324792, XM_166376, gen.NM_004973 gen.XM_166376 Figure 2040: PRO81422 Figure 2005: PRO81407 Figure 2041: DNA324810, XM_167196, Figure 2006A-B: DNA324793, XM_165799, gen.XM_167196 gen.XM_165799 Figure 2042: DNA324811, XM_166446, Figure 2007: DNA290264, NM_025263, gen.XM_166446 gen.NM_025263 Figure 2043: PRO81424 Figure 2008: PRO70393 Figure 2044A-C: DNA324812, XM_165777. Figure 2009: DNA324794, XM_166361, gen.XM_165777 gen.XM_166361 Figure 2045: DNA324813, XM_037875, Figure 2010: PRO81409 gen.XM_037875 Figure 2011: DNA324795, XM_165764, Figure 2046: PRO81426 gen.XM_165764 Figure 2047: DNA324814, XM_167225, Figure 2012: PRO81410 gen.XM_167225 Figure 2013: DNA324796, XM_165758, Figure 2048: PRO81427 gen.XM_165758 Figure 2049: DNA324815, XM_166357. Figure 2014: PRO81411 gen.XM_166357 Figure 2015: DNA324797, XM_166406. Figure 2050: DNA324816, NM_001069, gen.XM_166406 gen.NM_001069 Figure 2016: DNA324798, XM_165809, Figure 2051: PRO81429 gen.XM_165809 Figure 2052: DNA324817, NM_001500. Figure 2017: DNA324799, NM_018950. gen.NM_001500

Figure 2053: PRO81430 Figure 2087: DNA324839, XM_167016, Figure 2054A-B: DNA324818, XM_166042, gen.XM_167016 gen.XM_166042 Figure 2088: PRO81449 Figure 2055: PRO51389 Figure 2089: DNA324840, XM_087855, Figure 2056: DNA324819, XM_052721, gen.XM_087855 gen.XM_052721 Figure 2090: DNA324841, XM_087853, Figure 2057: DNA324820, XM_165499, gen.XM_087853 gen.XM_165499 Figure 2091: DNA324842, XM_165669, Figure 2058: DNA324821, XM_114497, gen.XM_165669 gen.XM_114497 Figure 2092: DNA324843, XM_166303, Figure 2059: DNA324822, XM_011117, gen.XM_166303 gen.XM_011117 Figure 2093: PRO81453 Figure 2060: DNA324823, XM_094855, Figure 2094: DNA324844, XM_167027, gen.XM_094855 gen.XM_167027 Figure 2061: PRO81435 Figure 2095: PRO81454 Figure 2062: DNA324824, XM_059776, Figure 2096: DNA324845, XM_167037, gen.XM_059776 gen.XM_167037 Figure 2063: PRO81436 Figure 2097: PRO81455 Figure 2064: DNA324825, XM_055641, Figure 2098: DNA324846, XM_018182, gen.XM_055641 gen.XM_018182 Figure 2065: DNA324826, XM_004151, Figure 2099: DNA227924, NM_000165, gen.XM_004151 gen.NM_000165 Figure 2066: DNA324827, NM_133645, Figure 2100: PRO38387 gen.NM_133645 Figure 2101: DNA324847, XM_166310, Figure 2067: PRO81439 gen.XM_166310 Figure 2068: DNA324828, XM_097453, Figure 2102: PRO81457 gen.XM_097453 Figure 2103: DNA324848, XM_168054, Figure 2069: DNA324829, XM_029228, gen.XM_168054 gen.XM_029228 Figure 2104: DNA271418, NM_003287, Figure 2070: DNA103471, NM_006670, gen.NM_003287 gen.NM_006670 Figure 2105: PRO59717 Figure 2071: PRO4798 Figure 2106: DNA324849, XM_114492, Figure 2072: DNA324830, XM_068963, gen.XM_114492 gen.XM_068963 Figure 2107: DNA324850, XM_037056, Figure 2073: PRO81441 gen.XM_037056 Figure 2074: DNA324831, XM _040623, Figure 2108: DNA324851, XM_098468, gen.XM_040623 gen.XM_098468 Figure 2075: DNA324832, NM_020320, Figure 2109: PRO19933 gen.NM_020320 Figure 2110: DNA324852, XM_004526, Figure 2076: PRO81443 gen.XM_004526 Figure 2077: DNA324833, NM_014107, Figure 2111: DNA324853, NM_001016, gen.NM_014107 gen.NM_001016 Figure 2078: PRO81444 Figure 2112: PRO81462 Figure 2079A-B: DNA324834, XM_084204, Figure 2113: DNA324854, XM_004297, gen.XM_084204 gen.XM_004297 Figure 2080: DNA324835, XM_017517, Figure 2114: DNA324855, XM_004256, gen.XM_017517 gen.XM_004256 Figure 2081: DNA324836, NM_032929. Figure 2115: PRO81464 gen.NM_032929 Figure 2116: DNA324856, NM_014320, Figure 2082: PRO81446 gen.NM_014320 Figure 2083: DNA324837, XM_003611, Figure 2117: PRO81465 gen.XM_003611 Figure 2118: DNA324857, XM_059741, Figure 2084: PRO81447 gen.XM_059741 Figure 2085: DNA324838, XM_068919, Figure 2119: DNA324858, XM_017831, gen.XM_068919 gen.XM_017831 Figure 2086: PRO81448 Figure 2120: PRO81467

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Figure 2328: DNA324977, XM_167483, gen.NM_057089 gen.XM_167483 Figure 2364: PRO81588 Figure 2329: DNA324978, XM_167484, Figure 2365: DNA324995, NM_001283, gen.XM_167484 gen.NM_001283 Figure 2330: PRO81572 Figure 2366: PRO41882 Figure 2331: DNA324979, NM _030935, Figure 2367: DNA324996, NM _003378, gen.NM_030935 gen.NM_003378 Figure 2332: PRO81573 Figure 2368: PRO81589 Figure 2333: DNA324980, NM_019606. Figure 2369: DNA324997, NM _001084, gen.NM_019606 gen.NM_001084 Figure 2334: PRO81574 Figure 2370: PRO58437 Figure 2335: DNA324981, NM_024070, Figure 2371: DNA270711, NM_006349, gen.NM_024070 gen.NM_006349 Figure 2336: PRO81575 Figure 2372: PRO59074 Figure 2337: DNA324982, XM_084241, Figure 2373: DNA324998, NM_024653, gen.XM_084241 gen.NM_024653 Figure 2338: DNA324983, NM_006833, Figure 2374: PRO81590 gen.NM_006833 Figure 2375: DNA324999, XM_168548, Figure 2339: PRO22897 gen.XM_168548 Figure 2340: DNA324984, NM_032164, Figure 2376: DNA325000, NM_032958, gen.NM_032164 gen.NM_032958 Figure 2341: PRO81578 Figure 2377: PRO81591 Figure 2342: DNA304801, NM_004889, Figure 2378: DNA325001, NM_002803, gen.NM_004889 gen.NM_002803 Figure 2343: PRO71211 Figure 2379: PRO81592 Figure 2344: DNA324985, NM _006693, Figure 2380: DNA325002, XM_168572, gen.NM_006693 gen.XM_168572 Figure 2345: PRO81579 Figure 2381: DNA325003, XM_071605. Figure 2346: DNA324986, XM_165839, gen.XM_071605 gen.XM_165839 Figure 2382: PRO81594 Figure 2347: PRO81580 Figure 2383: DNA325004, XM_033876, Figure 2348: DNA272090, NM_005720, gen.XM_033876 gen.NM_005720 Figure 2384: PRO81595 Figure 2349: PRO60360 Figure 2385A-B: DNA325005, XM_027214, Figure 2350: DNA324987, XM_165836, gen.XM_027214 gen.XM_165836 Figure 2386: DNA325006, XM_088073, Figure 2351A-B: DNA324988, XM_166482, gen.XM_088073 gen.XM_166482 Figure 2387: DNA325007, XM_072430, Figure 2352: DNA324989, XM_088180, gen.XM_072430 gen.XM_088180 Figure 2388: PRO81598 Figure 2353A-B: DNA324990, XM_166485, Figure 2389: DNA325008, XM_050430, gen.XM_166485 gen.XM_050430 Figure 2354: PRO81584 Figure 2390: PRO81599 Figure 2355: DNA324991, NM_001673, Figure 2391: DNA325009, NM_001753, gen.NM_001673 gen.NM_001753 Figure 2356: PRO81585 Figure 2392: PRO81600 Figure 2357: DNA324992, NM_133436, Figure 2393: DNA226560, NM_006136, gen.NM_133436 gen.NM_006136 Figure 2358: PRO81586 Figure 2394: PRO37023 Figure 2359: DNA324993, XM_168586, Figure 2395: DNA325010, XM_012284, gen.XM_168586 gen.XM_012284 Figure 2360: PRO81587 Figure 2396: DNA325011, NM_005000, Figure 2361: DNA83141, NM_000602, gen.NM_005000 gen.NM.000602 Figure 2397: PRO59380 Figure 2362: PRO2604 Figure 2398: DNA325012, NM_001662, Figure 2363: DNA324994, NM_057089, gen.NM_001662

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Figure 2399: PRO39773 gen.XM_016700 Figure 2400: DNA325013, XM_011618, Figure 2434: DNA325035, XM_042781, gen.XM_011618 gen.XM_042781 Figure 2401: PRO81602 Figure 2435: DNA304685, NM _003143. Figure 2402: DNA325014, XM_004627, gen.NM_003143 gen.XM_004627 Figure 2436: PRO71111 Figure 2403: DNA325015, XM_045401, Figure 2437: DNA325036, NM_018238, gen.XM_045401 gen.NM_018238 Figure 2404: DNA325016, XM_114602, Figure 2438: PRO81625 gen.XM_114602 Figure 2439: DNA325037, XM_035107, Figure 2405: PRO81605 gen.XM_035107 Figure 2406: DNA325017, XM_117481, Figure 2440: DNA325038, NM_003461, gen.XM_117481 gen.NM_003461 Figure 2407A-C: DNA325018, XM_045856, Figure 2441: PRO10194 gen.XM_045856 Figure 2442: DNA325039, NM_004911, Figure 2408: PRO81607 gen.NM_004911 Figure 2409A-B: DNA325019, XM_088105, Figure 2443: PRO2733 gen.XM_088105 Figure 2444A-B: DNA325040, XM_114578, Figure 2410: PRO81608 gen.XM_114578 Figure 2411: DNA325020, XM_011548, Figure 2445: PRO81627 gen.XM_011548 Figure 2446: DNA325041, XM_088135, Figure 2412: PRO81609 gen.XM_088135 Figure 2413: DNA325021, XM_045952, Figure 2447: DNA325042, XM_098654. gen.XM_045952 gen.XM_098654 Figure 2414: DNA325022, XM_046001, Figure 2448: PRO81629 gen.XM_046001 Figure 2449: DNA325043, NM_023942, Figure 2415: PRO81611 gen.NM_023942 Figure 2416: DNA325023, XM_088099 Figure 2450: PRO81630 gen.XM_088099 Figure 2451: DNA325044, NM_138434, Figure 2417: DNA325024, XM_040498, gen.NM_138434 gen.XM_040498 Figure 2452: PRO81631 Figure 2418: DNA325025, XM_088103, Figure 2453: DNA325045, XM_084238, gen.XM_088103 gen.XM_084238 Figure 2419: PRO81614 Figure 2454A-B: DNA325046, XM_032216, Figure 2420: DNA325026, XM_088122, gen.XM_032216 gen.XM_088122 Figure 2455A-B: DNA325047, XM_032121, Figure 2421: PRO81615 gen.XM_032121 Figure 2422: DNA325027, XM_088119, Figure 2456: DNA325048, NM_031434, gen.XM_088119 gen.NM_031434 Figure 2423: DNA325028, NM_001628, Figure 2457: PRO1555 gen.NM_001628 Figure 2458: DNA226337, NM_005692, Figure 2424: PRO81617 gen.NM_005692 Figure 2425: DNA325029, NM_020299, Figure 2459: PRO36800 gen.NM_020299 Figure 2460: DNA325049, NM_005614, Figure 2426: PRO81618 gen.NM_005614 Figure 2427: DNA325030, NM_024033, Figure 2461: PRO37938 gen.NM_024033 Figure 2462A-B: DNA325050, NM_053043, Figure 2428: PRO81619 gen.NM_053043 Figure 2429: DNA325031, XM_114555, Figure 2463: PRO81634 gen.XM_114555 Figure 2464: DNA325051, NM_022458, Figure 2430: DNA325032, XM_059839, gen.NM_022458 gen.XM_059839 Figure 2465: PRO81635 Figure 2431: PRO81621 Figure 2466: DNA325052, XM_098669, Figure 2432: DNA325033, XM_095146, gen.XM_098669 gen.XM_095146 Figure 2467: DNA325053, NM_017760, Figure 2433: DNA325034, XM_016700, gen.NM_017760

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Figure 2537: PRO81668

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Figure 2710: DNA325188, XM_018006, Figure 2674: PRO59579 gen.XM_018006 Figure 2675: DNA325174, NM_013442, Figure 2711: DNA325189, XM_017996, gen.NM_013442 gen.XM_017996 Figure 2676: PRO9819 Figure 2677: DNA325175, XM_114661, Figure 2712: DNA325190, XM_016113, gen.XM_016113 gen.XM_114661 Figure 2713: PRO81751 Figure 2678: PRO81736 Figure 2679: DNA325176, XM_048479, Figure 2714: DNA272655, NM_001827, gen.NM_001827 gen.XM_048479 Figure 2680: DNA290319, NM_003289, Figure 2715: PRO60781 Figure 2716A-B: DNA325191, NM_002161, gen.NM_003289 Figure 2681: PRO70595 gen.NM_002161 Figure 2682A-C: DNA325177, NM_006289, Figure 2717: PRO81752 gen.NM_006289 Figure 2718A-B: DNA325192, NM_013417, gen.NM_013417 Figure 2683: PRO81738 Figure 2684: DNA325178, XM_048518, Figure 2719: PRO81753 Figure 2720A-B: DNA325193, XM _046863, gen.XM_048518 gen.XM_046863 Figure 2685: PRO81739 Figure 2721: PRO81754 Figure 2686: DNA325179, XM_048539, Figure 2722: DNA325194, XM_046836, gen.XM_048539 gen.XM_046836 Figure 2687: PRO81740 Figure 2723: DNA275322, NM_003837, Figure 2688: DNA325180, XM_114662, gen.NM_003837 gen.XM_114662 Figure 2689: DNA325181, NM _001833, Figure 2724: PRO63000 Figure 2725A-B: DNA325195, XM _098943, gen.NM_001833 gen.XM_098943 Figure 2690: PRO81742 Figure 2726: DNA325196, XM_016308, Figure 2691: DNA227491, NM_007096, gen.NM_007096 gen.XM_016308 Figure 2692: PRO37954 Figure 2727: DNA325197, XM_005525, gen.XM_005525 Figure 2693: DNA254771, NM_012203, Figure 2728: DNA325198, NM _003389, gen.NM_012203 gen.NM_003389 Figure 2694: PRO49869 Figure 2729: PRO81759 Figure 2695: DNA89242, NM_000700, Figure 2730: DNA325199, NM_033219, gen.NM_000700 gen.NM_033219 Figure 2696: PRO2907 Figure 2731: PRO81760 Figure 2697: DNA325182, XM_041020, Figure 2732: DNA325200, NM_006401, gen.XM_041020 gen.NM_006401 Figure 2698: PRO81743 Figure 2733: PRO81761 Figure 2699: DNA325183, XM_114686, Figure 2734: DNA272213, NM_002486, gen.XM_114686 Figure 2700: DNA325184, XM_088637, gen.NM_002486 Figure 2735: PRO60475 gen.XM_088637 Figure 2736: DNA325201, NM_001333, Figure 2701: DNA287216, NM_021154, gen.NM_001333 gen.NM_021154 Figure 2737: PRO81762 Figure 2702: PRO69496 Figure 2738: DNA325202, XM_116818, Figure 2703: DNA288247, NM_058179, gen.XM_116818 gen.NM_058179 Figure 2739: PRO81763 Figure 2704: PRO70011 Figure 2705: DNA325185, XM_071178, Figure 2740: DNA254543, NM_006808, gen.NM_006808 gen.XM_071178 Figure 2741: PRO49648 Figure 2706: PRO81746 Figure 2742: DNA325203, XM_070873, Figure 2707: DNA325186, XM_005490, gen.XM_070873 gen.XM_005490 Figure 2743: PRO81764 Figure 2708: DNA325187, NM_031263, Figure 2744: DNA325204, XM_042788, gen.NM_031263 gen.XM_042788

Figure 2709: PRO81748

Figure 2745: PRO81765 Figure 2779: PRO81780 Figure 2746: DNA257309, NM_032342, Figure 2780: DNA325222, NM_000976, gen.NM_032342 gen.NM_000976 Figure 2747: PRO51901 Figure 2781: PRO62236 Figure 2748: DNA325205, XM_088569, Figure 2782: DNA218841, NM_012098, gen.XM_088569 gen.NM_012098 Figure 2749: PRO81766 Figure 2783: PRO34473 Figure 2750: DNA325206, XM_088571, Figure 2784A-B: DNA325223, XM_052725, gen.XM_088571 gen.XM_052725 Figure 2751: DNA271722, NM_004697, Figure 2785: PRO81781 gen.NM_004697 Figure 2786: DNA325224, XM_011752, Figure 2752: PRO60006 gen.XM_011752 Figure 2753: DNA325207, NM_017443, Figure 2787: DNA325225, XM_026944, gen.NM_017443 gen.XM_026944 Figure 2754: PRO81768 Figure 2788: PRO81783 Figure 2755A-C: DNA325208, XM_005348, Figure 2789: DNA325226, XM_116806, gen.XM_005348 gen.XM_116806 Figure 2756: DNA325209, XM_114646, Figure 2790A-B: DNA325227, NM _005347, gen.XM_114646 gen.NM_005347 Figure 2757: DNA325210, XM_038391, Figure 2791: PRO81785 gen.XM_038391 Figure 2792: DNA325228, NM_005833, Figure 2758: PRO81771 gen.NM_005833 Figure 2759A-B: DNA325211, XM_045296, Figure 2793: PRO81786 gen.XM_045296 Figure 2794: DNA325229, NM_007209, Figure 2760: DNA325212, XM_005365, gen.NM_007209 gen.XM_005365 Figure 2795: PRO61897 Figure 2761: DNA289530, NM_004435, Figure 2796: DNA88350, NM_000177, gen.NM_004435 gen.NM_000177 Figure 2762: PRO70290 Figure 2797: PRO2758 Figure 2763: DNA287271, NM_032799, Figure 2798A-B: DNA325230, XM_011749, gen.NM_032799 gen.XM_011749 Figure 2764: PRO69542 Figure 2799: DNA325231, XM_114679, Figure 2765: DNA325213, XM_026987, gen.XM_114679 gen.XM_026987 Figure 2800: DNA325232, XM_087041, Figure 2766: DNA325214, XM_026985, gen.XM_087041 gen.XM_026985 Figure 2801: DNA325233, XM_114678, Figure 2767: DNA225630, NM_016174, gen.XM_114678 gen.NM_016174 Figure 2802: DNA325234, XM_114677. Figure 2768: PRO36093 gen.XM_114677 Figure 2769: DNA325215, XM_026968, Figure 2803: DNA325235, XM_087038, gen.XM_026968 gen.XM_087038 Figure 2770: PRO81775 Figure 2804: DNA325236, XM_059637, Figure 2771: DNA325216, XM_026951, gen.XM_059637 gen.XM_026951 Figure 2805: PRO81792 Figure 2772: DNA325217, NM_025072, Figure 2806: DNA325237, NM_000368, gen.NM_025072 gen.NM_000368 Figure 2773: PRO33818 Figure 2807: PRO60115 Figure 2774: DNA325218, XM_033424, Figure 2808: DNA325238, XM_033385, gen.XM_033424 gen.XM_033385 Figure 2775: DNA325219, NM_004957, Figure 2809A-B: DNA325239, XM_033380, gen.NM_004957 gen.XM_033380 Figure 2776: PRO81778 Figure 2810: PRO81794 Figure 2777: DNA325220, XM_033457, Figure 2811: DNA325240, XM_033362, gen.XM_033457 gen.XM_033362 Figure 2778A-B: DNA325221, XM_033460. Figure 2812: PRO81795 gen.XM_033460 Figure 2813: DNA325241, XM_059986,

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Figure 2882: PRO62617 Figure 2917: PRO81849 Figure 2883: DNA325285, NM_003739, Figure 2918: DNA325305, XM_166665, gen.NM_003739 gen.XM_166665 Figure 2884: PRO81832 Figure 2919A-B: DNA325306, NM_002211. Figure 2885: DNA325286, XM_060976, gen.NM_002211 gen.XM_060976 Figure 2920: PRO81851 Figure 2886: PRO81833 Figure 2921A-B: DNA325307, XM_165567. Figure 2887: DNA325287, XM_167626, gen.XM_165567 gen.XM_167626 Figure 2922: DNA325308, XM_166157. Figure 2888: PRO81834 gen.XM_166157 Figure 2889: DNA325288, XM_165555, Figure 2923: DNA325309, NM_032023. gen.XM_165555 gen.NM_032023 Figure 2890: PRO81835 Figure 2924: PRO52537 Figure 2891: DNA325289, NM_001494, Figure 2925: DNA325310, XM_165560, gen.NM_001494 gen.XM_165560 Figure 2892: PRO81836 Figure 2926: DNA325311, XM_165563, Figure 2893: DNA325290, NM_032905. gen.XM_165563 gen.NM_032905 Figure 2927: DNA325312, XM_113615, Figure 2894: PRO81837 gen.XM_113615 Figure 2895: DNA325291, NM_005174, Figure 2928: PRO81855 gen.NM_005174 Figure 2929: DNA325313, XM_165890, Figure 2896: PRO81838 gen.XM_165890 Figure 2897: DNA325292, XM_165557, Figure 2930: DNA325314, XM_061126, gen.XM_165557 gen.XM_061126 Figure 2898: DNA325293, XM_167374, Figure 2931: DNA325315, XM_061125, gen.XM_167374 gen.XM_061125 Figure 2899: DNA273759, NM_006023, Figure 2932: PRO81858 gen.NM_006023 Figure 2933: DNA325316, XM_054474, Figure 2900: PRO61721 gen.XM_054474 Figure 2901: DNA325294, XM_167411, Figure 2934: DNA325317, XM_165888, gen.XM_167411 gen.XM_165888 Figure 2902: DNA325295, NM_031453, Figure 2935: DNA325318, XM _054475, gen.NM_031453 gen.XM_054475 Figure 2903: PRO81841 Figure 2936: PRO81861 Figure 2904: DNA325296, XM_167414, Figure 2937: DNA325319, XM_015652. gen.XM_167414 gen.XM_015652 Figure 2905: PRO12851 Figure 2938: PRO81862 Figure 2906: DNA325297, XM_166717, Figure 2939: DNA325320, XM_036593, gen.XM_166717 gen.XM_036593 Figure 2907: PRO81842 Figure 2940: PRO81863 Figure 2908: DNA325298, XM_005100, Figure 2941: DNA325321, XM_165891, gen.XM_005100 gen.XM_165891 Figure 2909: DNA325299, XM_038536, Figure 2942: DNA325322, XM_084450, gen.XM_038536 gen.XM_084450 Figure 2910A-B: DNA325300, XM_084420, Figure 2943: PRO81865 gen.XM_084420 Figure 2944: DNA325323, XM_084385, Figure 2911: DNA325301, XM_084429. gen.XM_084385 gen.XM_084429 Figure 2945: DNA325324, NM_021226, Figure 2912: PRO81846 gen.NM_021226 Figure 2913A-C: DNA325302, XM_165551, Figure 2946: PRO81867 gen.XM_165551 Figure 2947: DNA193957, NM_003055, Figure 2914: DNA325303, XM_059720, gen.NM_003055 gen.XM_059720 Figure 2948: PRO23364 Figure 2915: PRO81848 Figure 2949: DNA325325, NM_032997, Figure 2916A-B: DNA325304, NM_019619, gen.NM_032997 gen.NM_019619 Figure 2950: PRO81868

Figure 2951: DNA287642, NM_018464, gen.NM_005729 gen.NM_018464 Figure 2987: PRO37073 Figure 2952: PRO9902 Figure 2988: DNA325342, XM_166629, Figure 2953: DNA325326, XM_084451, gen.XM_166629 gen.XM_084451 Figure 2989: PRO81883 Figure 2954: PRO81869 Figure 2990: DNA103506, NM_001157, Figure 2955: DNA325327, NM_012207, gen.NM_001157 gen.NM_012207 Figure 2991: PRO4833 Figure 2956: PRO81870 Figure 2992: DNA325343, XM_016093, Figure 2957: DNA325328, NM _024045, gen.XM_016093 gen.NM_024045 Figure 2993: PRO81884 Figure 2958: PRO81871 Figure 2994: DNA325344, XM_084467, Figure 2959: DNA325329, NM_004728, gen.XM_084467 gen.NM_004728 Figure 2995: PRO81885 Figure 2960: PRO81872 Figure 2996: DNA304488, NM_032333, Figure 2961: DNA88562, NM_002727, gen.NM_032333 gen.NM_002727 Figure 2997: PRO71057 Figure 2962: PRO2842 Figure 2998: DNA325345, XM_043589, Figure 2963: DNA325330, XM_167395, gen.XM_043589 gen.XM_167395 Figure 2999: DNA325346, XM_043605, Figure 2964: DNA227172, NM_021129, gen.XM_043605 gen.NM_021129 Figure 3000: DNA325347, XM_087480, Figure 2965: PRO37635 gen.XM_087480 Figure 2966A-B: DNA325331, XM_166125, Figure 3001: PRO81887 gen.XM_166125 Figure 3002: DNA325348, NM_002921, Figure 2967: PRO81874 gen.NM_002921 Figure 2968: DNA325332, XM_044354, Figure 3003: PRO81888 gen.XM_044354 Figure 3004: DNA226217, NM_005271, Figure 2969: PRO81875 gen.NM_005271 Figure 2970: DNA325333, XM_032520, Figure 3005: PRO36680 gen.XM_032520 Figure 3006: DNA325349, XM_089551, Figure 2971: DNA325334, NM_019058, gen.XM_089551 gen.NM_019058 Figure 3007: PRO81889 Figure 2972: PRO81877 Figure 3008: DNA287237, NM_001613, Figure 2973: DNA325335, XM_045140, gen.NM_001613 gen.XM_045140 Figure 3009: PRO39648 Figure 2974: PRO2875 Figure 3010: DNA325350, XM_084477, Figure 2975: DNA325336, XM_116863, gen.XM_084477 gen.XM_116863 Figure 3011: PRO69523 Figure 2976: DNA325337, XM_032476, Figure 3012: DNA325351, XM_084480, gen.XM_032476 gen.XM_084480 Figure 2977: DNA325338, XM_114894, Figure 3013A-B: DNA325352, NM_013451, gen.XM_114894 gen.NM_013451 Figure 2978: DNA325339, NM_033022, Figure 3014: PRO12813 Figure 3015: DNA325353, XM_018167, gen.NM_033022 Figure 2979: PRO81881 gen.XM_018167 Figure 2980: DNA325340, NM_001026, Figure 3016: DNA325354, XM_084372, gen.NM_001026 gen.XM_084372 Figure 3017: DNA325355, NM_020992, Figure 2981: PRO11139 Figure 2982: DNA103421, NM_003375, gen.NM_020992 gen.NM_003375 Figure 3018: PRO81893 Figure 2983: PRO4749 Figure 3019: DNA325356, XM_089514, Figure 2984A-B: DNA325341, XM_166093, gen.XM_089514 gen.XM_166093 Figure 3020A-B: DNA325357, XM_058343, Figure 2985: PRO81882 gen.XM_058343

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Figure 2986: DNA304459, NM_005729,

Figure 3022: DNA325358, XM_058602, Figure 3058A-B: DNA325377, XM _005938, gen.XM_058602 gen.XM_005938 Figure 3023: PRO81896 Figure 3059A-B: DNA325378, XM _031992, Figure 3024A-B: DNA325359, NM_015179, gen.XM_031992 gen.NM_015179 Figure 3060: PRO81912 Figure 3025: PRO81897 Figure 3061: DNA325379, NM_032747, Figure 3026: DNA325360, XM_083842, gen.NM_032747 gen.XM_083842 Figure 3062: PRO81913 Figure 3027: PRO69473 Figure 3063: DNA325380, NM_005004, Figure 3028: DNA325361, XM_084413, gen.NM_005004 gen.XM_084413 Figure 3064: PRO81914 Figure 3029: DNA325362, NM_022362, Figure 3065: DNA325381, XM_030447, gen.NM_022362 gen.XM_030447 Figure 3030: PRO81899 Figure 3066: DNA273521, NM_002079, Figure 3031: DNA325363, NM_032112, gen.NM_002079 gen.NM_032112 Figure 3067: PRO61502 Figure 3032: PRO81900 Figure 3068A-B: DNA325382, NM_032211, Figure 3033: DNA325364, NM_021830, gen.NM_032211 gen.NM_021830 Figure 3069: PRO81916 Figure 3034: PRO81901 Figure 3070: DNA325383, NM_031484, Figure 3035A-B: DNA325365, XM_046743, gen.NM_031484 gen.XM_046743 Figure 3071: PRO81917 Figure 3036: PRO81902 Figure 3072: DNA325384, XM_084632, Figure 3037: DNA325366, NM_013274, gen.XM_084632 gen.NM_013274 Figure 3073: DNA325385, XM_084359, Figure 3038: PRO81903 gen.XM_084359 Figure 3039: DNA325367, NM_022039, Figure 3074A-D: DNA325386, XM_045667, gen.NM_022039 gen.XM_045667 Figure 3040: PRO81904 Figure 3075: DNA325387, XM_109162, Figure 3041A-B: DNA325368, XM_031866, gen.XM_109162 gen.XM_031866 Figure 3076: DNA227509, NM_000274, Figure 3042A-B: DNA325369, NM_015062, gen.NM_000274 gen.NM_015062 Figure 3077: PRO37972 Figure 3043: PRO81905 Figure 3078: DNA325388, XM_058361, Figure 3044A-B: DNA325370, XM_031890, gen.XM_058361 gen.XM_031890 Figure 3079: PRO81922 Figure 3045A-B: DNA325371, NM_004193, Figure 3080: DNA325389, XM_084505, gen.NM_004193 gen.XM_084505 Figure 3046: PRO81907 Figure 3081: PRO81923 Figure 3047: DNA325372, NM_024040, Figure 3082A-B: DNA325390, XM_049795, gen.NM_024040 gen.XM_049795 Figure 3048: PRO81908 Figure 3083: PRO81924 Figure 3049: DNA325373, XM_031949, Figure 3084: DNA325391, XM_058406, gen.XM_031949 gen.XM_058406 Figure 3050: PRO4900 Figure 3085: PRO81925 Figure 3051A-B: DNA144601, NM_016169. Figure 3086: DNA325392, XM_055573, gen.NM_016169 gen.XM_055573 Figure 3052: PRO34073 Figure 3087: PRO60991 Figure 3053: DNA325374, XM_005698, Figure 3088: DNA325393, XM_005969, gen.XM_005698 gen.XM_005969 Figure 3054: PRO81909 Figure 3089: DNA325394, NM_007190, Figure 3055: DNA325375, NM_006523, gen.NM_007190 gen.NM_006523 Figure 3090: PRO81926 Figure 3056: PRO59043 Figure 3091: DNA325395, NM_000982, Figure 3057: DNA325376, XM_018279, gen.NM_000982 gen.XM_018279 Figure 3092: PRO81927

Figure 3093: DNA269952, NM_004725, Figure 3129: DNA325412, XM_044932, gen.NM_004725 gen.XM_044932 Figure 3094: PRO58348 Figure 3130: PRO81943 Figure 3095: DNA325396, NM_024942, Figure 3131A-B: DNA325413, XM_044957, gen.NM_024942 gen.XM_044957 Figure 3096: PRO81928 Figure 3132: PRO81944 Figure 3097: DNA325397, NM_016567, Figure 3133: DNA325414, NM_001909, gen.NM_016567 gen.NM_001909 Figure 3098: PRO81929 Figure 3134: PRO292 Figure 3099: DNA325398, NM_004092, Figure 3135: DNA325415, XM_006475, gen.NM_004092 gen.XM_006475 Figure 3100: PRO81930 Figure 3136: DNA325416, XM_006483, Figure 3101: DNA269431, NM_006659, gen.XM_006483 gen.NM_006659 Figure 3137: DNA325417, NM_001751, Figure 3102: PRO57854 gen.NM_001751 Figure 3103: DNA325399, XM_005675, Figure 3138: PRO69635 gen.XM_005675 Figure 3139: DNA325418, XM_114981, Figure 3104: DNA325400, XM_114862, gen.XM_114981 gen.XM_114862 Figure 3140: PRO81945 Figure 3105: PRO81932 Figure 3141: DNA325419, XM_083852, Figure 3106: DNA325401, XM_088009, gen.XM_083852 gen.XM_088009 Figure 3142: DNA325420, NM_000559, Figure 3107: DNA325402, NM_016526, gen.NM_000559 gen.NM_016526 Figure 3143: PRO81946 Figure 3108: PRO81934 Figure 3144: DNA325421, NM_000184, Figure 3109: DNA255696, NM_021932, gen.NM_000184 gen.NM_021932 Figure 3145: PRO81947 Figure 3110: PRO50756 Figure 3146: DNA325422, NM_005330, Figure 3111: DNA325403, XM_043220, gen.NM_005330 gen.XM_043220 Figure 3147: PRO81948 Figure 3112: PRO81935 Figure 3148: DNA325423, XM_015243, Figure 3113: DNA255078, NM_006435, gen.XM_015243 gen.NM_006435 Figure 3149: DNA325424, NM_015324, Figure 3114: PRO50165 gen.NM_015324 Figure 3115: DNA325404, NM_002339, Figure 3150: PRO81950 gen.NM_002339 Figure 3151: DNA325425, XM_006424, Figure 3116: PRO81936 gen.XM_006424 Figure 3117: DNA325405, XM_028192, Figure 3152: DNA325426, XM_113238, gen.XM_028192 gen.XM_113238 Figure 3118: PRO81937 Figure 3153A-C: DNA325427, XM_052786, Figure 3119: DNA325406, XM_096544, gen.XM_052786 gen.XM_096544 Figure 3154: PRO81953 Figure 3120: DNA325407, NM_000612, Figure 3155: DNA325428, NM_000990. gen.NM_000612 gen.NM_000990 Figure 3121: PRO124 Figure 3156: PRO25985 Figure 3122: DNA325408, XM_084742, Figure 3157A-B: DNA325429, XM_045750, gen.XM_084742 gen.XM_045750 Figure 3123: PRO81939 Figure 3158: PRO81954 Figure 3124: DNA325409, XM_084739, Figure 3159: DNA325430, XM_058414, gen.XM_084739 gen.XM_058414 Figure 3125: DNA325410, XM_058505. Figure 3160: PRO81955 gen.XM_058505 Figure 3161A-B: DNA325431, XM_049197, Figure 3126: PRO81941 gen.XM_049197 Figure 3127: DNA325411, XM_006139, Figure 3162: PRO81956 gen.XM_006139 Figure 3163A-B: DNA325432, NM_001418, Figure 3128: PRO81942 gen.NM_001418

Figure 3164: PRO81957 gen.NM_003646 Figure 3165: DNA325433, XM_096520, Figure 3198: PRO81977 gen.XM_096520 Figure 3199: DNA325455, NM_004551, Figure 3166: PRO81958 gen.NM_004551 Figure 3167: DNA325434, XM_006212. Figure 3200: PRO81978 gen.XM_006212 Figure 3201: DNA325456, XM_006170, Figure 3168: PRO81959 gen.XM_006170 Figure 3169: DNA325435, XM_084527. Figure 3202: DNA325457, XM_037173, gen.XM_084527 gen.XM_037173 Figure 3170: DNA325436, XM_016139, Figure 3203: PRO81980 gen.XM_016139 Figure 3204: DNA150974, NM_005693. Figure 3171: DNA325437, NM_001017. gen.NM_005693 gen.NM_001017 Figure 3205: PRO12224 Figure 3172: PRO11262 Figure 3206: DNA226080, NM_001610, Figure 3173: DNA325438, NM_014267, gen.NM_001610 gen.NM_014267 Figure 3207: PRO36543 Figure 3174: PRO81962 Figure 3208: DNA270134, NM_000107, Figure 3175: DNA97285, NM_005566, gen.NM_000107 gen.NM_005566 Figure 3209: PRO58523 Figure 3176: PRO3632 Figure 3210: DNA325458, NM_016223, Figure 3177: DNA325439, XM_115081, gen.NM_016223 gen.XM_115081 Figure 3211: PRO81981 Figure 3178: DNA325440, XM_036339. Figure 3212: DNA325459, XM_037147, gen.XM_036339 gen.XM_037147 Figure 3179: PRO81964 Figure 3213: PRO81982 Figure 3180: DNA325441, XM_084514, Figure 3214: DNA325460, XM_015705, gen.XM_084514 gen.XM_015705 Figure 3181: PRO81965 Figure 3215: DNA272728, NM_003146, Figure 3182: DNA325442, XM_084516, gen.NM_003146 gen.XM_084516 Figure 3216: PRO60847 Figure 3183: DNA325443, XM_084515, Figure 3217: DNA325461, XM_165611, gen.XM_084515 gen.XM_165611 Figure 3184: DNA325444, XM_084517, Figure 3218: DNA287417, NM_024098, gen.XM_084517 gen.NM_024098 Figure 3185: DNA325445, XM_034431, Figure 3219: PRO69674 gen.XM_034431 Figure 3220: DNA227088, NM_014502, Figure 3186: PRO11691 gen.NM_014502 Figure 3187: DNA325446, XM_030326, Figure 3221: PRO37551 gen.XM_030326 Figure 3222: DNA325462, XM_165610, Figure 3188: DNA325447, NM_057174, gen.XM_165610 gen.NM_057174 Figure 3223A-B: DNA325463, XM_165612, Figure 3189: PRO81970 gen.XM_165612 Figure 3190: DNA325448, NM_004813, Figure 3224: DNA325464, XM_166234. gen.NM_004813 gen.XM_166234 Figure 3191: PRO81971 Figure 3225: DNA325465, NM_015533, Figure 3192: DNA325449, XM_167437, gen.NM_015533 gen.XM_167437 Figure 3226: PRO81988 Figure 3193: DNA325450, XM_054856. Figure 3227: DNA325466, XM_166232, gen.XM_054856 gen.XM_166232 Figure 3194: DNA325451, XM_004330, Figure 3228A-B: DNA325467, XM_167748, gen.XM_004330 gen.XM_167748 Figure 3195: DNA325452, XM_084681, Figure 3229: PRO81990 gen.XM_084681 Figure 3230: DNA325468, NM_004739, Figure 3196: DNA325453, XM _006297, gen.NM_004739 gen.XM_006297 Figure 3231: PRO81991 Figure 3197: DNA325454, NM_003646. Figure 3232: DNA325469, NM_014610,

gen.NM_014610 Figure 3268: DNA325488, XM_113223, Figure 3233: PRO81992 gen.XM_113223 Figure 3234: DNA325470, XM_167747, Figure 3269: DNA325489, XM_045642, gen.XM_167747 gen.XM_045642 Figure 3235: PRO81993 Figure 3270: DNA325490, XM_006533, Figure 3236: DNA287254, NM_024099, gen.XM_006533 gen.NM_024099 Figure 3271: DNA325491, XM_045613, Figure 3237: PRO69528 gen.XM_045613 Figure 3238: DNA325471, NM_015853. Figure 3272: PRO59721 gen.NM_015853 Figure 3273A-B: DNA325492, XM_045612, Figure 3239: PRO81994 gen.XM_045612 Figure 3240: DNA325472, NM_032667. Figure 3274: PRO82009 gen.NM_032667 Figure 3275: DNA325493, XM_113224, Figure 3241: PRO81995 gen.XM_113224 Figure 3242: DNA325473, NM _006362, Figure 3276: DNA325494, XM_045499, gen.NM_006362 gen.XM_045499 Figure 3243: PRO81996 Figure 3277: PRO82011 Figure 3244: DNA325474, XM_167716, Figure 3278: DNA325495, XM _045525, gen.XM_167716 gen.XM_045525 Figure 3245: DNA75863, NM_002411, Figure 3279: DNA325496, NM_013265, gen.NM_002411 gen.NM_013265 Figure 3246: PRO2018 Figure 3280: PRO82013 Figure 3247: DNA325475, XM_087710, Figure 3281: DNA325497, XM_006529, gen.XM_087710 gen.XM_006529 Figure 3248: DNA325476, XM_167726, Figure 3282: PRO60008 gen.XM_167726 Figure 3283: DNA325498, XM_053787, Figure 3249: DNA325477, NM_004265, gen.XM_053787 gen.NM_004265 Figure 3284: DNA269803, NM_001667, Figure 3250: PRO12878 gen.NM_001667 Figure 3251A-B: DNA325478, NM_013402, Figure 3285: PRO58207 gen.NM_013402 Figure 3286: DNA325499, XM_115031, Figure 3252: PRO81999 gen.XM_115031 Figure 3253: DNA325479, NM_004111, Figure 3287: DNA325500, XM_084702, gen.NM_004111 gen.XM_084702 Figure 3254: PRO69568 Figure 3288: DNA325501, XM_053796, Figure 3255: DNA325480, XM_048286, gen.XM_053796 gen.XM_048286 Figure 3289: DNA325502, NM _002689, Figure 3256: DNA325481, NM_004322, gen.NM_002689 gen.NM_004322 Figure 3290: PRO82018 Figure 3257: PRO20117 Figure 3291A-D: DNA325503, XM_167804, Figure 3258: DNA325482, NM_032989, gen.XM_167804 gen.NM_032989 Figure 3292: PRO82019 Figure 3259: PRO20117 Figure 3293: DNA325504, XM_166235, Figure 3260: DNA325483, XM_011988, gen.XM_166235 gen.XM_011988 Figure 3294: DNA325505, XM_166236, Figure 3261: DNA325484, NM_031472, gen.XM_166236 gen.NM_031472 Figure 3295: DNA270721, NM_006842, Figure 3262: PRO82002 gen.NM_006842 Figure 3263: DNA325485, XM_037808, Figure 3296: PRO59084 gen.XM_037808 Figure 3297: DNA189687, NM_000852, Figure 3264: DNA325486, NM_004074, gen.NM_000852 gen.NM_004074 Figure 3298: PRO25845 Figure 3265: PRO82004 Figure 3299: DNA325506, NM_007103, Figure 3266: DNA325487, NM_017670, gen.NM_007103 gen.NM_017670 Figure 3300: PRO58606 Figure 3267: PRO82005 Figure 3301: DNA325507, NM_005851,

gen.NM_005851 gen.XM_166253 Figure 3302: PRO69461 Figure 3337: DNA325526, NM_001293, Figure 3303A-B: DNA325508, XM_165598, gen.NM_001293 gen.XM_165598 Figure 3338: PRO82034 Figure 3304: DNA325509, NM_006019. Figure 3339: DNA325527, XM_042852, gen.NM_006019 gen.XM_042852 Figure 3305: PRO82023 Figure 3340: PRO82035 Figure 3306: DNA325510, NM_006053, Figure 3341: DNA325528, XM_165628, gen.NM_006053 gen.XM_165628 Figure 3307: PRO24831 Figure 3342A-B: DNA325529, NM_080491. Figure 3308: DNA325511, XM_166196, gen.NM_080491 gen.XM_166196 Figure 3343: PRO82037 Figure 3309: PRO82024 Figure 3344A-B: DNA325530, NM_012296, Figure 3310: DNA325512, XM_165600, gen.NM_012296 gen.XM_165600 Figure 3345: PRO60311 Figure 3311A-B: DNA325513, NM_053056, Figure 3346: DNA325531, NM_032379, gen.NM_053056 gen.NM_032379 Figure 3312: PRO4870 Figure 3347: PRO82038 Figure 3313: DNA103474, NM_003824, Figure 3348: DNA325532, NM_007173, gen.NM_003824 gen.NM_007173 Figure 3314: PRO4801 Figure 3349: DNA325533, XM_166239, Figure 3315: DNA325514, XM_096486, gen.XM_166239 gen.XM_096486 Figure 3350: DNA325534, XM_084610, Figure 3316A-B: DNA325515, NM_003626, gen.XM_084610 gen.NM_003626 Figure 3351: PRO82040 Figure 3317: PRO82027 Figure 3352: DNA325535, XM_058450, Figure 3318A-B: DNA325516, XM_167853, gen.XM_058450 gen.XM_167853 Figure 3353: DNA325536, XM_084601, Figure 3319: PRO82028 gen.XM_084601 Figure 3320: DNA325517, NM_014042, Figure 3354: PRO82042 gen.NM_014042 Figure 3355A-B: DNA325537, XM_006464, Figure 3321: PRO82029 gen.XM_006464 Figure 3322A-B: DNA325518, NM_001567, Figure 3356: PRO82043 gen.NM_001567 Figure 3357: DNA325538, XM_084570, Figure 3323: PRO61238 gen.XM_084570 Figure 3324: DNA325519, XM_167433, Figure 3358: DNA325539, XM_051435, gen.XM_167433 gen.XM_051435 Figure 3325: DNA325520, XM_165616, Figure 3359: DNA325540, NM_001467. gen.XM_165616 gen.NM_001467. Figure 3326: DNA325521, NM_032871. Figure 3360: PRO82045 gen.NM_032871 Figure 3361: DNA325541, NM_001028, Figure 3327: PRO57307 gen.NM_001028 Figure 3328: DNA325522, XM_165631, Figure 3362: PRO82046 gen.XM_165631 Figure 3363: DNA325542, XM_113230, Figure 3329: DNA254186, NM_014752. gen.XM_113230 gen.NM_014752 Figure 3364: DNA325543, XM_115062, Figure 3330: PRO49298 gen.XM_115062 Figure 3331: DNA325523, NM_001005, Figure 3365: DNA325544, XM_115063, gen.NM_001005 gen.XM_115063 Figure 3332: PRO82032 Figure 3366: DNA325545, XM_113229, Figure 3333: DNA88176, NM_001235, gen.XM_113229 gen.NM_001235 Figure 3367A-B: DNA325546, XM_051489, Figure 3334: PRO2685 gen.XM_051489 Figure 3335A-B: DNA325524, XM_165627, Figure 3368: PRO82050 gen.XM_165627 Figure 3369: DNA325547, NM_022003. Figure 3336: DNA325525, XM_166253, gen.NM_022003

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Figure 3370: PRO82051 Figure 3405: PRO82066 Figure 3371: DNA325548, XM _006432. Figure 3406: DNA325565, XM_166177, gen.XM_006432 gen.XM_166177 Figure 3372: PRO82052 Figure 3407: DNA325566, XM_165571, Figure 3373: DNA325549, XM_051716, gen.XM_165571 gen.XM_051716 Figure 3408: PRO82068 Figure 3374: DNA325550, NM_025164, Figure 3409: DNA325567, XM_166174, gen.NM_025164 gen.XM_166174 Figure 3375: PRO82054 Figure 3410: PRO82069 Figure 3376: DNA225752, NM_000039, Figure 3411: DNA325568, NM _001274, gen.NM_000039 gen.NM_001274 Figure 3377: PRO36215 Figure 3412: PRO12187 Figure 3378: DNA325551, XM_052113, Figure 3413: DNA325569, XM_165586, gen.XM_052113 gen.XM_165586 Figure 3379: PRO82055 Figure 3414: DNA325570, XM_165584, Figure 3380: DNA271324, NM_006169, gen.XM_165584 gen.NM_006169 Figure 3415: DNA257965, NM_032873, Figure 3381: PRO59629 gen.NM_032873 Figure 3382: DNA325552, XM_084658. Figure 3416: PRO52492 gen.XM_084658 Figure 3417: DNA325571, XM_167780, Figure 3383: PRO82056 gen.XM_167780 Figure 3384: DNA325553, NM_000795, Figure 3418: DNA325572, XM_166743, gen.NM_000795 gen.XM_166743 Figure 3385: PRO12448 Figure 3419: PRO82072 Figure 3386: DNA325554, NM_017868, Figure 3420: DNA325573, NM_012101, gen.NM_012101 gen.NM_017868 Figure 3421: PRO82073 Figure 3387: PRO82057 Figure 3388: DNA325555, XM_084654, Figure 3422: DNA325574, NM_058193, gen.XM_084654 gen.NM_058193 Figure 3389: PRO82058 Figure 3423: PRO82074 Figure 3390: DNA272413, NM_003002, Figure 3424: DNA325575, XM_084522, gen.NM_003002 gen.XM_084522 Figure 3391: PRO60666 Figure 3425: PRO82075 Figure 3392: DNA271843, NM _004398, Figure 3426: DNA325576, XM_091786, gen.NM_004398 gen.XM_091786 Figure 3393: PRO60123 Figure 3427: DNA325577, XM_165390, Figure 3394: DNA325556, XM_017369, gen.XM_165390 gen.XM_017369 Figure 3428: DNA325578, XM_084525, Figure 3395: DNA325557, NM _032299, gen.XM_084525 gen.NM_032299 Figure 3429A-B: DNA325579, XM_010494, Figure 3396: PRO82060 gen.XM_010494 Figure 3397: DNA325558, XM_055369, Figure 3430A-B: DNA325580, NM_015064, gen.XM_055369 gen.NM_015064 Figure 3398: DNA325559, XM_051430, Figure 3431: PRO82078 gen.XM_051430 Figure 3432: DNA325581, NM_030775, Figure 3399: DNA325560, XM _006467, gen.NM_030775 gen.XM_006467 Figure 3433: PRO71031 Figure 3434: DNA297398, NM_032642, Figure 3400: DNA325561, XM_113226, gen.XM_113226 gen.NM_032642 Figure 3401: DNA325562, XM_165592, Figure 3435: PRO71031 gen.XM_165592 Figure 3436: DNA325582, XM_017080, Figure 3402: PRO82064 gen.XM_017080 Figure 3403: DNA325563, XM_166181, Figure 3437: DNA325583, XM_113739, gen.XM_166181 gen.XM_113739 Figure 3404: DNA325564, XM_052862, Figure 3438: PRO82080 gen.XM_052862 Figure 3439: DNA325584, NM_002014,

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Figure 3788A-B: DNA325766, XM_084941, gen.NM_014868 Figure 3824: PRO59042 gen.XM_084941 Figure 3789: PRO82237 Figure 3825: DNA325787, XM_052893, Figure 3790A-B: DNA325767, NM_057169, gen.XM_052893 gen.NM_057169 Figure 3826A-B: DNA325788, XM_045802, Figure 3791: PRO82238 gen.XM_045802 Figure 3792A-B: DNA325768, NM_014776, Figure 3827: DNA302016, NM _001002, gen.NM_001002 gen.NM_014776 Figure 3828: PRO70989 Figure 3793: PRO82239 Figure 3829: DNA325789, NM_053275, Figure 3794: DNA325769, NM _032904, gen.NM_032904 gen.NM_053275 Figure 3795: PRO82240 Figure 3830: PRO70989 Figure 3796A-B: DNA325770, XM_007003, Figure 3831: DNA325790, NM _006253, gen.NM_006253 gen.XM_007003 Figure 3797: DNA325771, XM_007002, Figure 3832: PRO82259 Figure 3833: DNA325791, XM_045187, gen.XM_007002 Figure 3798: DNA325772, XM_056996, gen.XM_045187 Figure 3834: DNA325792, XM_045963, gen.XM_056996 Figure 3799: PRO82243 gen.XM_045963 Figure 3835: DNA325793, XM_006595, Figure 3800: DNA325773, XM_084946, gen.XM_006595 gen.XM_084946 Figure 3801: PRO82244 Figure 3836: DNA325794, XM_012124, Figure 3802: DNA325775, XM_027102, gen.XM_012124 gen.XM_027102 Figure 3837: DNA325795, NM_002813, Figure 3803: PRO82245 gen.NM_002813 Figure 3838: PRO82263 Figure 3804: DNA325776, XM _084948, gen.XM_084948 Figure 3839: DNA325796, NM_019887, Figure 3805: DNA325777, NM _007062, gen.NM_019887 gen.NM_007062 Figure 3840: PRO69471 Figure 3806: PRO82247 Figure 3841A-B: DNA325797, XM_038791, Figure 3807: DNA325778, NM _006825, gen.XM_038791 Figure 3842: PRO82264 gen.NM_006825 Figure 3808: PRO82248 Figure 3843: DNA325798, NM_016638, Figure 3809: DNA325779, XM_115197, gen.NM_016638 gen.XM_115197 Figure 3844: PRO82265 Figure 3810: DNA325780, NM_017901, Figure 3845: DNA325799, XM_116913, gen.XM_116913 gen.NM_017901 Figure 3811: PRO82250 Figure 3846: PRO82266 Figure 3812: DNA325781, NM_032814, Figure 3847: DNA325800, NM _006815, gen.NM_006815 gen.NM_032814 Figure 3848: PRO4793 Figure 3813: PRO82252 Figure 3814: DNA325782, XM_084889, Figure 3849: DNA325801, XM_006566, gen.XM_084889 gen.XM_006566 Figure 3815: PRO82253 Figure 3850: PRO82267 Figure 3851: DNA325802, NM _032656, Figure 3816: DNA325783, NM_002567, gen.NM_002567 gen.NM_032656 Figure 3817: PRO59001 Figure 3852: PRO82268 Figure 3818: DNA325784, XM_084808, Figure 3853: DNA325803, XM_055013, gen.XM_084808 gen.XM_055013 Figure 3819: DNA325785, XM_096572, Figure 3854: PRO82269 Figure 3855: DNA325804, XM_113737, gen.XM_096572 Figure 3820: PRO82255 gen.XM_113737 Figure 3821: DNA325786, XM_045010, Figure 3856A-C: DNA325805, XM_045602, gen.XM_045010 gen.XM_045602 Figure 3822: PRO82256 Figure 3857: DNA325806, XM_087955, Figure 3823: DNA270677, NM_014868, gen.XM_087955

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Figure 3927: PRO82305 Figure 3961: PRO82325 Figure 3928: DNA325844, XM_041473, Figure 3962: DNA210180, NM_005132, gen.XM_041473 gen.NM_005132 Figure 3929: PRO82306 Figure 3963: PRO33717 Figure 3930: DNA325845, XM_032443, Figure 3964: DNA325867, XM_033337, gen.XM_032443 gen.XM_033337 Figure 3931: DNA325847, XM_048957, Figure 3965: PRO82326 gen.XM_048957 Figure 3966: DNA325868, XM _096772, Figure 3932: DNA325848, XM_015842, gen.XM_096772 gen.XM_015842 Figure 3967: DNA325869, XM_007293. Figure 3933: DNA325849, XM _084997. gen.XM_007293 gen.XM_084997 Figure 3968: DNA325870, XM_007288, Figure 3934: PRO82311 gen.XM_007288 Figure 3935: DNA325850, NM_024089, Figure 3969A-B: DNA325871, XM_033391, gen.NM_024089 gen.XM_033391 Figure 3936: PRO82312 Figure 3970: PRO82329 Figure 3937A-B: DNA325851, XM_049904, Figure 3971: DNA325872, NM_017815, gen.XM_049904 gen.NM_017815 Figure 3938: DNA325852, NM_024537, Figure 3972: PRO82330 gen.NM_024537 Figure 3973: DNA325873, NM_006109, Figure 3939: PRO82314 gen.NM_006109 Figure 3940: DNA325853, NM_023011, Figure 3974: PRO82331 gen.NM_023011 Figure 3975: DNA325874, XM_033435, Figure 3941: PRO82315 gen.XM_033435 Figure 3942: DNA325854, NM_080687, Figure 3976: DNA225865, NM_004995, gen.NM_080687 gen.NM_004995 Figure 3943: PRO82316 Figure 3977: PRO36328 Figure 3944: DNA325855, XM_041484, Figure 3978: DNA325875, XM_058647, gen.XM_041484 gen.XM_058647 Figure 3945: PRO82317 Figure 3979: PRO82333 Figure 3946A-B: DNA325856, XM_113752, Figure 3980: DNA325876, XM_033445, gen.XM_113752 gen.XM_033445 Figure 3947: PRO82318 Figure 3981: DNA325877, NM_005015, Figure 3948: DNA325857, XM_115215, gen.NM_005015 gen.XM_115215 Figure 3982: PRO82334 Figure 3949: DNA325858, XM_046651. Figure 3983: DNA325878, XM_012377, gen.XM_046651 gen.XM_012377 Figure 3950: DNA325859, XM_046648, Figure 3984: DNA227321, NM_001344. gen.XM_046648 gen.NM_001344 Figure 3951: DNA325860, XM_046642, Figure 3985: PRO37784 gen.XM_046642 Figure 3986: DNA325879, XM_058646, Figure 3952: PRO10404 gen.XM_058646 Figure 3953: DNA325861, XM_017914, Figure 3987: DNA325880, XM_085106, gen.XM_017914 gen.XM_085106 Figure 3954: PRO82321 Figure 3988: DNA325881, NM_019852, Figure 3955: DNA325862, XM_085166, gen.NM_019852 gen.XM_085166 Figure 3989: PRO82338 Figure 3956: PRO82322 Figure 3990: DNA325882, XM_012376, Figure 3957: DNA325863, XM_007316, gen.XM_012376 gen.XM_007316 Figure 3991: DNA325883, XM_033553, Figure 3958: DNA325864, XM_007315. gen.XM_033553 gen.XM_007315 Figure 3992: DNA226105, NM_002934, Figure 3959: DNA325865, XM_033251. gen.NM_002934 gen.XM_033251 Figure 3993: PRO36568 Figure 3960: DNA325866, NM_024658, Figure 3994: DNA325884, XM_033595, gen.NM_024658 gen.XM_033595

Figure 3995: PRO2871 Figure 4031: DNA325905, XM_085125, Figure 3996: DNA325885, XM_007491, gen.XM_085125 gen.XM_007491 Figure 4032: DNA325906, XM_031025, Figure 3997: DNA325886, NM_001641, gen.XM_031025 gen.NM_001641 Figure 4033: DNA325907, XM_085066, Figure 3998: PRO82342 gen.XM_085066 Figure 3999: DNA325887, NM_080648, Figure 4034: DNA325908, XM_096744, gen.NM_080648 gen.XM_096744 Figure 4000: PRO82343 Figure 4035: DNA325909, NM_016445. Figure 4001: DNA325888, NM_080649, gen.NM_016445 gen.NM_080649 Figure 4036: PRO82364 Figure 4002: PRO82344 Figure 4037: DNA325910, NM_016026. Figure 4003: DNA325889, NM_017807. gen.NM_016026 gen.NM_017807 Figure 4038: PRO82365 Figure 4004: PRO82345 Figure 4039: DNA325911, XM_031074, Figure 4005A-C: DNA325890, XM_007488, gen.XM_031074 gen.XM_007488 Figure 4040: DNA325912, NM_001102, Figure 4006: DNA325891, NM_021178, gen.NM_001102 gen.NM_021178 Figure 4041: PRO82367 Figure 4007: PRO82347 Figure 4042: DNA225649, NM_022137, Figure 4008: DNA325892, XM_041235, gen.NM_022137 gen.XM_041235 Figure 4043: PRO36112 Figure 4009: PRO82348 Figure 4044: DNA325913, XM_085065, Figure 4010: DNA325893, NM_002028. gen.XM_085065 gen.NM_002028 Figure 4045: DNA325914, XM_007441, Figure 4011: PRO82349 gen.XM_007441 Figure 4012: DNA325894, NM_002083, Figure 4046: DNA325915, NM_006821, gen.NM_002083 gen.NM_006821 Figure 4013: PRO82350 Figure 4047: PRO82369 Figure 4014A-B: DNA325895, XM_085127, Figure 4048: DNA325916, NM _006432, gen.XM_085127 gen.NM_006432 Figure 4015: PRO82351 Figure 4049: PRO2066 Figure 4016A-B: DNA325896, NM_001530, Figure 4050A-B: DNA325917, XM_085151, gen.NM_001530 gen.XM_085151 Figure 4017: PRO82352 Figure 4051: PRO82370 Figure 4018: DNA325897, XM_058210, Figure 4052: DNA325918, NM_002632, gen.XM_058210 gen.NM_002632 Figure 4019: DNA325898, XM_085141, Figure 4053: PRO82371 gen.XM_085141 Figure 4054: DNA325919, XM_085162, Figure 4020: DNA325899, NM_021728, gen.XM_085162 gen.NM_021728 Figure 4055: DNA325920, NM_012111. Figure 4021: PRO82355 gen.NM_012111 Figure 4022: DNA325900, NM_002306, Figure 4056: PRO82373 gen.NM_002306 Figure 4057: DNA325921, NM_024824, Figure 4023: PRO82356 gen.NM_024824 Figure 4024: DNA325901, XM_007328, Figure 4058: PRO82374 gen.XM_007328 Figure 4059: DNA269498, NM_002802, Figure 4025A-B: DNA325902, XM_051712, gen.NM_002802 gen.XM_051712 Figure 4060: PRO57917 Figure 4026: PRO82357 Figure 4061: DNA325922, XM_058677, Figure 4027: DNA325903, XM_007324, gen.XM_058677 gen.XM_007324 Figure 4062: PRO82375 Figure 4028: PRO82358 Figure 4063: DNA325923, NM_006888, Figure 4029: DNA325904, NM_002863, gen.NM_006888 gen.NM_002863 Figure 4064: PRO4904 Figure 4030: PRO82359 Figure 4065: DNA325924, NM _001275,

gen.NM_001275 Figure 4099: PRO82391 Figure 4066: PRO2054 Figure 4100: DNA325945, XM_040898, Figure 4067: DNA325925, XM _029288, gen.XM_040898 gen.XM_029288 Figure 4101: DNA325946, NM_005432, Figure 4068A-B: DNA325926, XM_016487, gen.NM_005432 gen.XM_016487 Figure 4102: PRO60070 Figure 4069: DNA325927, NM_020414, Figure 4103A-B: DNA325947, XM_050278, gen.NM_020414 gen.XM_050278 Figure 4070: PRO62099 Figure 4104: PRO82393 Figure 4071: DNA325928, XM_016486, Figure 4105: DNA325948, XM_113759, gen.XM_016486 gen.XM_113759 Figure 4072: DNA325929, XM_007483, Figure 4106: DNA325949, NM_006427, gen.XM_007483 gen.NM_006427 Figure 4073: DNA325930, XM _028358, Figure 4107: PRO82395 gen.XM_028358 Figure 4108: DNA325950, NM_021709, Figure 4074: DNA325931, XM_028347, gen.NM_021709 Figure 4109: PRO82396 gen.XM_028347 Figure 4075: DNA325932, XM _028322, Figure 4110: DNA103509, NM_005163, gen.XM_028322 gen.NM_005163 Figure 4076: PRO82381 Figure 4111: PRO4836 Figure 4077: DNA325933, XM_056317, Figure 4112: DNA325951, NM_017955, gen.XM_056317 gen.NM_017955 Figure 4078: PRO82382 Figure 4113: PRO82397 Figure 4079: DNA151893, NM_021966, Figure 4114: DNA325952, XM_088588, gen.NM_021966 gen.XM_088588 Figure 4080: PRO12916 Figure 4115: DNA325953, XM_060012, Figure 4081: DNA325934, XM_007272, gen.XM_060012 gen.XM_007272 Figure 4116: DNA325954, XM_034953, Figure 4082: DNA325935, XM _090914, gen.XM_034953 gen.XM_090914 Figure 4117: PRO82400 Figure 4083: PRO82383 Figure 4118: DNA325955, XM_058636, Figure 4084: DNA325936, NM_022747, gen.XM_058636 gen.NM_022747 Figure 4119: DNA325956, XM_035014, Figure 4085: PRO82384 gen.XM_035014 Figure 4086: DNA325937, XM_041014, Figure 4120: DNA325957, XM_088587, gen.XM_041014 gen.XM_088587 Figure 4087: PRO60575 Figure 4121: DNA325958, XM_088589, Figure 4088: DNA325938, NM_003836, gen.XM_088589 gen.NM_003836 Figure 4122: DNA325959, XM_071801, Figure 4089: PRO82385 gen.XM_071801 Figure 4123: DNA325960, XM_018054. Figure 4090A-B: DNA325939, XM_040952, gen.XM_040952 gen.XM_018054 Figure 4124: DNA325961, XM_091108. Figure 4091: DNA325940, XM_058618, gen.XM_058618 gen.XM_091108 Figure 4092: DNA325941, NM_005348, Figure 4125A-B: DNA325962, XM_039225, gen.NM_005348 gen.XM_039225 Figure 4093: PRO82388 Figure 4126: PRO82408 Figure 4094: DNA325942, XM_040942, Figure 4127: DNA325963, XM_165921, gen.XM_040942 gen.XM_165921 Figure 4095: DNA226324, NM_014226, Figure 4128: PRO82409 gen.NM_014226 Figure 4129: DNA325964, XM_007751, Figure 4096: PRO36787 gen.XM_007751 Figure 4097A-B: DNA325943, XM_007254, Figure 4130: DNA325965, XM_085203, gen.XM_007254 gen.XM_085203 Figure 4098A-B: DNA325944, NM_001969, Figure 4131: PRO82411 gen.NM_001969 Figure 4132: DNA325966, XM_085204,

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Figure 4694: DNA326270, XM_008231, gen.XM_051763 gen.XM_008231 Figure 4728: DNA290292, NM_018955. Figure 4695: DNA326271, XM_113328, gen.NM_018955 gen.XM_113328 Figure 4729: PRO70449 Figure 4696: DNA326272, XM_113929, Figure 4730: DNA326289, XM_058900. gen.XM_113929 gen.XM_058900 Figure 4697: DNA326273, NM_001970, Figure 4731: PRO82691 gen.NM_001970 Figure 4732: DNA326290, XM_039921, Figure 4698: PRO82678 gen.XM_039921 Figure 4699: DNA297388, NM_004217, Figure 4733: PRO82692 gen.NM_004217 Figure 4734: DNA326291, XM_012549, Figure 4700: PRO70812 gen.XM_012549 Figure 4701: DNA326274, XM_165421, Figure 4735: DNA326292, XM_085548. gen.XM_165421 gen.XM_085548 Figure 4702: PRO82679 Figure 4736: PRO82694 Figure 4703: DNA326275, XM_113325, Figure 4737: DNA326293, NM_018019, gen.XM_113325 gen.NM_018019 Figure 4704: DNA326276, XM_165422, Figure 4738: PRO82695 gen.XM_165422 Figure 4739: DNA326294, NM_138427, Figure 4705: PRO49182 gen.NM_138427 Figure 4706: DNA326277, XM_113931, Figure 4740: PRO82696 gen.XM_113931 Figure 4741: DNA326295, XM _085545, Figure 4707: DNA326278, XM_036659, gen.XM_085545 gen.XM_036659 Figure 4742A-B: DNA227084, NM_004176. Figure 4708: DNA103401, NM_003876, gen.NM_004176 gen.NM_003876 Figure 4743: PRO37547 Figure 4709: PRO4729 Figure 4744: DNA326296, XM_012615, Figure 4710A-B: DNA326279, XM_042698, gen.XM_012615 gen.XM_042698 Figure 4745: DNA326297, XM_085722, Figure 4711: PRO82683 gen.XM_085722 Figure 4712A-B: DNA326280, XM_017234, Figure 4746: PRO82699 gen.XM_017234 Figure 4747: DNA255414, NM_018242, Figure 4713: DNA326281, XM_165418. gen.NM_018242 gen.XM_165418 Figure 4748: PRO50481 Figure 4714: DNA304715, NM_000987, Figure 4749: DNA326298, XM_045044, gen.NM_000987 gen.XM_045044 Figure 4715: PRO71141 Figure 4750: DNA326299, XM_008323, Figure 4716A-B: DNA326282, NM_004618, gen.XM_008323 gen.NM_004618 Figure 4751: DNA326300, XM_045535, Figure 4717: PRO62981 gen.XM_045535 Figure 4718: DNA326283, XM_085743, Figure 4752A-B: DNA326301, XM_045551, gen.XM_085743 gen.XM_045551 Figure 4719A-B: DNA254198, NM_002018. Figure 4753: PRO82702 gen.NM_002018 Figure 4754: DNA326302, XM_097204, Figure 4720: PRO49310 gen.XM_097204 Figure 4721A-B: DNA326284, XM_039910, Figure 4755: DNA326303, XM_058867, gen.XM_039910 gen.XM_058867 Figure 4722: PRO82687 Figure 4756: PRO82704 Figure 4723A-C: DNA326285, XM_113310, Figure 4757: DNA326304, XM_085672, gen.XM_113310 gen.XM_085672 Figure 4724: DNA326286, XM_085613, Figure 4758: DNA326305, XM_031536. gen.XM_085613 gen.XM_031536 Figure 4725: DNA326287, NM_006470, Figure 4759: PRO82706 gen.NM_006470 Figure 4760: DNA326306, XM_008486, Figure 4726: PRO82689 gen.XM_008486 Figure 4727: DNA326288, XM_051763, Figure 4761: DNA326307, NM_015584.

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gen.XM_054038 Figure 4868: PRO82754 Figure 4833: PRO82738 Figure 4869: DNA326359, XM_008402, Figure 4834: DNA326343, NM_002265, gen.XM_008402 gen.NM_002265 Figure 4870: PRO82755 Figure 4835: PRO82739 Figure 4871: DNA326360, NM_017595, Figure 4836: DNA326344, XM_032201, gen.NM_017595 gen.XM_032201 Figure 4872: PRO82756 Figure 4837: PRO82740 Figure 4873: DNA326361, XM_085636, Figure 4838: DNA326345, NM_012138, gen.XM_085636 gen.NM_012138 Figure 4874: PRO82757 Figure 4839: PRO82741 Figure 4875: DNA326362, NM_006373, Figure 4840: DNA326346, XM_018534, gen.NM_006373 gen.XM_018534 Figure 4876: PRO82758 Figure 4841: DNA227873, NM_001050, Figure 4877: DNA196642, NM_005440, gen.NM_001050 gen.NM_005440 Figure 4842: PRO38336 Figure 4878: PRO25115 Figure 4843: DNA270975, NM_000386. Figure 4879A-B: DNA270901, NM_004247, gen.NM_000386 gen.NM_004247 Figure 4844: PRO59305 Figure 4880: DNA326363, XM_050159, Figure 4845: DNA88378, NM_002087, gen.XM_050159 gen.NM_002087 Figure 4881: DNA326364, XM_083983, Figure 4846: PRO2769 gen.XM_083983 Figure 4847: DNA326347, NM_016016, Figure 4882: PRO82760 gen.NM_016016 Figure 4883A-B: DNA326365, NM_021079, Figure 4848: PRO82743 gen.NM_021079 Figure 4849: DNA326348, XM_012642, Figure 4884: PRO82761 gen.XM_012642 Figure 4885: DNA326366, NM_133373, Figure 4850A-B: DNA326349, NM_005474, gen.NM_133373 gen.NM_005474 Figure 4886: PRO82762 Figure 4851: PRO82745 Figure 4887: DNA97290, NM _002512, Figure 4852: DNA326350, XM_045901, gen.NM_002512 gen.XM_045901 Figure 4888: PRO3637 Figure 4853: PRO82746 Figure 4889: DNA227071, NM_000269, Figure 4854: DNA257428, NM_032376, gen.NM_000269 gen.NM_032376 Figure 4890: PRO37534 Figure 4855: PRO52010 Figure 4891: DNA227764, NM_003971, Figure 4856: DNA326351, XM _008351, gen.NM_003971 gen.XM_008351 Figure 4892: PRO38227 Figure 4857: DNA326352, XM_032852. Figure 4893A-B: DNA326367, NM _020038, gen.XM_032852 gen.NM_020038 Figure 4858: PRO82748 Figure 4894: PRO82763 Figure 4859: DNA326353, NM_025233, Figure 4895A-B: DNA326368, NM_020037, gen.NM_025233 gen.NM_020037 Figure 4860: PRO82749 Figure 4896: PRO82764 Figure 4861: DNA326354, XM_032817, Figure 4897: DNA326369, XM_037971, gen.XM_032817 gen.XM_037971 Figure 4862: PRO82750 Figure 4898: DNA254791, NM_018346, Figure 4863: DNA326355, XM_032813, gen.NM_018346 gen.XM_032813 Figure 4899: PRO49888 Figure 4864: DNA326356, XM_032766, Figure 4900: DNA287425, NM_018509. gen.XM_032766 gen.NM_018509 Figure 4865: DNA326357, NM_003766, Figure 4901: PRO69682 gen.NM_003766 Figure 4902A-B: DNA326370, XM_008432, Figure 4866: PRO82753 gen.XM_008432 Figure 4867: DNA326358, XM_008401, Figure 4903: DNA88554, NM_000250. gen.XM_008401 gen.NM_000250

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gen.XM_044367

gen.XM_054344 Figure 5007: PRO82813 Figure 4974: PRO82797 Figure 5008: DNA326429, NM_004127, Figure 4975: DNA274755, NM_002766. gen.NM_004127 gen.NM_002766 Figure 5009: PRO82814 Figure 4976: PRO70703 Figure 5010A-C: DNA326430, XM_113943, Figure 4977A-B: DNA326409, XM_085531, gen.XM_113943 gen.XM_085531 Figure 5011: DNA326431, XM_113330, Figure 4978: DNA326410, XM_113892, gen.XM_113330 gen.XM_113892 Figure 5012: PRO82816 Figure 4979: PRO82799 Figure 5013: DNA326432, XM_113303, Figure 4980: DNA326411, XM_017578, gen.XM_113303 gen.XM_017578 Figure 5014: DNA287234, NM _031968, Figure 4981: PRO82800 gen.NM_031968 Figure 4982: DNA326412, XM_036785, Figure 5015: PRO69513 gen.XM_036785 Figure 5016: DNA326433, NM_022158, Figure 4983: PRO39201 gen.NM_022158 Figure 4984: DNA326413, XM_097043, Figure 5017: PRO82818 gen.XM_097043 Figure 5018: DNA326434, XM_038424, Figure 4985: DNA129504, NM_001168, gen.XM_038424 gen.NM_001168 Figure 5019: DNA326435, XM_085735, Figure 4986: PRO7143 gen.XM_085735 Figure 4987: DNA326414, XM_037196, Figure 5020: DNA326436, XM_046765, gen.XM_037196 gen.XM_046765 Figure 4988: DNA326415, XM_037195, Figure 5021: DNA326437, XM_046769, gen.XM_037195 gen.XM_046769 Figure 4989: DNA326416, XM_045104, Figure 5022: DNA326438, XM_046767, gen.XM_045104 gen.XM_046767 Figure 4990: PRO37540 Figure 5023: DNA273694, NM_006101, Figure 4991: DNA326417, XM_085563, gen.NM_006101 gen.XM_085563 Figure 5024: PRO61661 Figure 4992A-B: DNA326418, XM_085716, Figure 5025A-B: DNA326439, XM_028744. gen.XM_085716 gen.XM_028744 Figure 4993: PRO82805 Figure 5026: DNA326440, XM_165954, Figure 4994A-B: DNA326419, XM_049934, gen.XM_165954 gen.XM_049934 Figure 5027: DNA326441, XM_041678. Figure 4995: DNA326420, XM_049931, gen.XM_041678 gen.XM_049931 Figure 5028: DNA326442, XM_113343, Figure 4996A-B: DNA326421, XM_045581, gen.XM_113343 gen.XM_045581 Figure 5029: PRO82825 Figure 4997: PRO82807 Figure 5030: DNA326443, XM_067325, Figure 4998: DNA326422, XM_113945. gen.XM_067325 gen.XM_113945 Figure 5031: DNA326444, XM_012741, Figure 4999: DNA326423, XM_046481, gen.XM_012741 gen.XM_046481 Figure 5032: DNA326445, NM_014214, Figure 5000: DNA326424, XM_097195, gen.NM_014214 gen.XM_097195 Figure 5033: PRO82828 Figure 5001: DNA326425, XM_097193, Figure 5034A-B: DNA326446, XM_035640, gen.XM_097193 gen.XM_035640 Figure 5002: DNA326426, NM_004309, Figure 5035: PRO82829 Figure 5036: DNA326447, XM_016382, gen.NM_004309 Figure 5003: PRO61246 gen.XM_016382 Figure 5004: DNA326427, XM_046472, Figure 5037: DNA326448, NM_032933, gen.XM_046472 gen.NM_032933 Figure 5005: PRO82812 Figure 5038: PRO82831 Figure 5006: DNA326428, NM_016286, Figure 5039: DNA274690, NM_006938, gen.NM_016286 gen.NM_006938

Figure 5040A-B: DNA88457, NM_000227, Figure 5074: DNA326467, XM _006937. gen.NM_000227 gen.XM_006937 Figure 5041: PRO2799 Figure 5075: DNA326468, XM_085779, Figure 5042: DNA326449, XM_085791, gen.XM_085779 gen.XM_085791 Figure 5076: DNA326469, XM_011089, Figure 5043: DNA326450, XM_085789, gen.XM_011089 gen.XM_085789 Figure 5077: PRO82850 Figure 5044: PRO82833 Figure 5078: DNA326470, XM_169540, Figure 5045: DNA326451, XM_085790, gen.XM_169540 gen.XM_085790 Figure 5079: PRO82851 Figure 5046: DNA326452, XM_015755, Figure 5080: DNA326471, XM_167008, gen.XM_015755 gen.XM_167008 Figure 5047: PRO82835 Figure 5081: PRO82852 Figure 5048: DNA326453, XM .097232, Figure 5082: DNA326472, XM_048471, gen.XM_097232 gen.XM_048471 Figure 5049: DNA326454, XM_085788, Figure 5083A-B: DNA326473, XM_008812, gen.XM_085788 gen.XM_008812 Figure 5050: DNA88281, NM_001944, Figure 5084A-B: DNA326474, XM_117096. gen.NM_001944 gen.XM_117096 Figure 5051: PRO2267 Figure 5085: PRO82855 Figure 5052: DNA271841, NM_003787, Figure 5086: DNA326475, NM_002385, gen.NM_003787 gen.NM_002385 Figure 5053: PRO60121 Figure 5087: PRO82856 Figure 5088: DNA326476, XM_015241, Figure 5054: DNA326455, XM_008723, gen.XM_008723 gen.XM_015241 Figure 5055: DNA326456, XM_084007, Figure 5089A-B: DNA326477, XM_008695, gen.XM_084007 gen.XM_008695 Figure 5056: DNA256813, NM_018255, Figure 5090A-B: DNA326478, XM_041872, gen.NM_018255 gen.XM_041872 Figure 5057: PRO51744 Figure 5091: PRO82859 Figure 5058: DNA326457, XM_085775, Figure 5092: DNA326479, XM_051586, gen.XM_085775 gen.XM_051586 Figure 5059: PRO82840 Figure 5093: DNA326480, NM_003712, Figure 5060: DNA326458, NM_138443, gen.NM_003712 gen.NM_138443 Figure 5094: PRO1077 Figure 5061: PRO82841 Figure 5095: DNA326481, XM_042018, Figure 5062: DNA326459, XM_038872, gen.XM_042018 gen.XM_038872 Figure 5096: PRO2560 Figure 5063: PRO82842 Figure 5097: DNA326482, XM_114018, Figure 5064: DNA326460, XM_086779, gen.XM_114018 gen.XM_086779 Figure 5098: DNA326483, NM_017876. Figure 5065: DNA326461, XM_167363, gen.NM_017876 gen.XM_167363 Figure 5099: PRO82861 Figure 5066: DNA326462, XM_031944, Figure 5100: DNA326484, NM_031990, gen.XM_031944 gen.NM_031990 Figure 5067: DNA326463, NM_000985, Figure 5101: PRO82862 gen.NM_000985 Figure 5102: DNA326485, NM_002819, Figure 5068: PRO82846 gen.NM_002819 Figure 5069: DNA326464, NM_002396, Figure 5103: PRO62899 gen.NM_002396 Figure 5104: DNA326486, NM_005224, Figure 5070: PRO61113 gen.NM_005224 Figure 5071: DNA326465, XM_166288, Figure 5105: PRO82863 gen.XM_166288 Figure 5106: DNA326487, XM_037565, Figure 5072: DNA326466, NM_004539, gen.XM_037565 gen.NM_004539 Figure 5107: PRO82864 Figure 5073: PRO60800 Figure 5108: DNA326488, XM_092042,

gen.XM_092042 Figure 5142: PRO82881 Figure 5109: DNA326489, XM_037572, Figure 5143: DNA326510, NM_017797, gen.XM_037572 gen.NM_017797 Figure 5110: DNA326490, XM_009279. Figure 5144: PRO82882 gen.XM_009279 Figure 5145: DNA326511, XM_030714, Figure 5111: PRO82867 gen.XM_030714 Figure 5112: DNA326491, NM_002085, Figure 5146: DNA256555, NM_017572, gen.NM_002085 gen.NM_017572 Figure 5113A-B: DNA326492, XM_009277, Figure 5147: PRO51586 gen.XM_009277 Figure 5148A-B: DNA326512, NM_003938, Figure 5114: DNA326493, XM_012913. gen.NM_003938 gen.XM_012913 Figure 5149: PRO82884 Figure 5115: DNA274101, NM_001687, Figure 5150A-B: DNA326513, XM_046822, gen.NM_001687 gen.XM_046822 Figure 5116: PRO62039 Figure 5151: PRO82885 Figure 5117: DNA326494, XM_028067, Figure 5152: DNA326514, NM_007165, gen.XM_028067 gen.NM_007165 Figure 5118: PRO82871 Figure 5153: PRO82886 Figure 5119: DNA326495, XM_028064, Figure 5154: DNA287636, NM_004152, gen.XM_028064 gen.NM_004152 Figure 5120: DNA326496, NM_024407. Figure 5155: DNA326515, NM_012458, gen.NM_024407 gen.NM_012458 Figure 5121: PRO82872 Figure 5156: PRO82887 Figure 5122: DNA326497, NM_000156, Figure 5157: DNA326516, NM_032737, gen.NM_000156 gen.NM_032737 Figure 5123: PRO58046 Figure 5158: PRO82888 Figure 5124: DNA326498, NM_138924, Figure 5159: DNA326517, XM_030485, gen.NM_138924 gen.XM_030485 Figure 5125: PRO82873 Figure 5160: DNA326518, XM_046934. Figure 5126: DNA326499, NM_001018, gen.XM_046934 gen.NM_001018 Figure 5161: DNA326519, NM_003021, Figure 5127: PRO10485 gen.NM_003021 Figure 5128: DNA326500, XM_086101, Figure 5162: PRO62302 gen.XM_086101 Figure 5163: DNA326520, XM_055686, Figure 5129: PRO82874 gen.XM_055686 Figure 5130: DNA326501, XM_086102, Figure 5164: PRO37951 gen.XM_086102 Figure 5165: DNA326521, XM_009222, Figure 5131: DNA326502, XM_047584. gen.XM_009222 gen.XM_047584 Figure 5166: DNA326522, XM_052635, Figure 5132A-B: DNA326503, XM_047600, gen.XM_052635 gen.XM_047600 Figure 5167: PRO82892 Figure 5133: PRO38496 Figure 5168: DNA326523, XM_052661, Figure 5134: DNA326504, XM_097420, gen.XM_052661 gen.XM_097420 Figure 5169: DNA326524, NM_016263, Figure 5135A-B: DNA326505, XM_030721. gen.NM_016263 gen.XM_030721 Figure 5170: PRO82893 Figure 5136: PRO82877 Figure 5171: DNA326525, NM_006339, Figure 5137: DNA326506, XM_030720. gen.NM_006339 gen.XM_030720 Figure 5172: PRO82894 Figure 5138: DNA326507, NM_031213, Figure 5173: DNA326526, NM_032753, gen.NM_031213 gen.NM_032753 Figure 5139: PRO82879 Figure 5174: PRO82895 Figure 5140: DNA326508, XM_039723, Figure 5175: DNA326527, XM_056421, gen.XM_039723 gen.XM_056421 Figure 5141: DNA326509, NM_001319. Figure 5176A-B: DNA326528, XM_031917, gen.NM_001319 gen.XM_031917

Figure 5177: PRO82897 gen.XM_012798 Figure 5178: DNA326529, NM_001961, Figure 5213: DNA326548, XM_044608, gen.NM_001961 gen.XM_044608 Figure 5179: PRO62225 Figure 5214: DNA326549, NM_003624, Figure 5180: DNA326530, XM_016871, gen.NM_003624 gen.XM_016871 Figure 5215: PRO82915 Figure 5181: DNA326531, NM_016539. Figure 5216: DNA326550, NM_016579, gen.NM_016539 gen.NM_016579 Figure 5182: PRO82899 Figure 5217: PRO224 Figure 5183: DNA326532, XM_117122, Figure 5218A-B: DNA326551, XM_048351, gen.XM_117122 gen.XM_048351 Figure 5184: DNA326533, XM_031857, Figure 5219: DNA326552, XM_048364, gen.XM_031857 gen.XM_048364 Figure 5185: PRO82901 Figure 5220: PRO82917 Figure 5186: DNA326534, NM_024333, Figure 5221: DNA326553, XM_091938, gen.NM_024333 gen.XM_091938 Figure 5187: PRO82902 Figure 5222: DNA326554, XM_097300, Figure 5188: DNA326535, NM_003025, gen.XM_097300 gen.NM_003025 Figure 5223: DNA326555, XM_049282, Figure 5189: PRO82903 gen.XM_049282 Figure 5190: DNA326536, NM_025241, Figure 5224: PRO82920 gen.NM_025241 Figure 5225: DNA326556, XM_058232, Figure 5191: PRO82904 gen.XM_058232 Figure 5192: DNA326537, XM_035638. Figure 5226: DNA326557, XM_045151, gen.XM_035638 gen.XM_045151 Figure 5193: PRO82905 Figure 5227A-B: DNA326558, XM_050435, Figure 5194A-B: DNA326538, XM_035636, gen.XM_050435 gen.XM_035636 Figure 5228: PRO82923 Figure 5195: DNA326539, XM_012862. Figure 5229: DNA326559, XM_113988, gen.XM_012862 gen.XM_113988 Figure 5196A-B: DNA326540, XM_035627. Figure 5230: DNA326560, NM_058164, gen.XM_035627 gen.NM_058164 Figure 5197A-B: DNA326541, XM ..035625, Figure 5231: PRO82925 gen.XM_035625 Figure 5232: DNA227280, NM_020230, Figure 5198: PRO82909 gen.NM_020230 Figure 5199: DNA274761, NM_014649, Figure 5233: PRO37743 gen.NM_014649 Figure 5234: DNA270621, NM_003755, Figure 5200: PRO62531 gen.NM_003755 Figure 5201: DNA272421, NM_006012, Figure 5235: PRO58991 gen.NM_006012 Figure 5236: DNA326561, XM_049502, Figure 5202: PRO60674 gen.XM_049502 Figure 5203: DNA326542, NM_003685, Figure 5237: DNA326562, NM_007065, gen.NM_003685 gen.NM_007065 Figure 5204: PRO82910 Figure 5238: PRO63226 Figure 5205A-B: DNA326543, XM_009010, Figure 5239: DNA326563, XM_049561, gen.XM_009010 gen.XM_049561 Figure 5206: DNA270315, NM_004240, Figure 5240: DNA326564, XM_017204, gen.NM_004240 gen.XM_017204 Figure 5207: PRO58702 Figure 5241: DNA326565, NM_005498, Figure 5208: DNA326544, NM_005490, gen.NM_005498 gen.NM_005490 Figure 5242: PRO62112 Figure 5209: PRO201 Figure 5243: DNA326566, XM_008887, Figure 5210: DNA326546, XM_044619, gen.XM_008887 gen.XM_044619 Figure 5244: DNA326567, XM_085862, Figure 5211: PRO82912 gen.XM_085862 Figure 5212: DNA326547, XM_012798, Figure 5245: PRO82930

Figure 5246: DNA326568, XM_084014, Figure 5280: PRO69518 gen.XM_084014 Figure 5281: DNA326586, XM_032020, Figure 5247A-B: DNA326569, XM_032710, gen.XM_032020 gen.XM_032710 Figure 5282: PRO2718 Figure 5248: DNA326570, XM_032719, Figure 5283: DNA326587, NM _005053, gen.XM_032719 gen.NM_005053 Figure 5249: PRO82933 Figure 5284: PRO22613 Figure 5250: DNA326571, NM_024029, Figure 5285: DNA326588, XM_085916, gen.NM_024029 gen.XM_085916 Figure 5251: PRO23794 Figure 5286: DNA326589, NM_017722, Figure 5252: DNA326572, XM_032724, gen.NM_017722 gen.XM_032724 Figure 5287: PRO82947 Figure 5253: PRO82934 Figure 5288: DNA326590, NM_003765, Figure 5254A-B: DNA326573, NM_003072, gen.NM_003765 gen.NM_003072 Figure 5289: PRO82948 Figure 5255: PRO82935 Figure 5290: DNA326591, XM_051364, Figure 5256A-B: DNA326574, XM_009082, gen.XM_051364 gen.XM_009082 Figure 5291: PRO82949 Figure 5257: DNA326575, XM_032774, Figure 5292: DNA326592, XM_031345, gen.XM_032774 gen.XM_031345 Figure 5258: DNA218271, NM_000121, Figure 5293: PRO82950 gen.NM_000121 Figure 5294: DNA326593, XM_113352, Figure 5259: PRO34323 gen.XM_113352 Figure 5260: DNA326576, XM ..057074, Figure 5295: DNA326594, XM_058967, gen.XM_057074 gen.XM_058967 Figure 5261: DNA326577, XM_032782, Figure 5296: PRO82952 Figure 5297: DNA326595, XM_085909, gen.XM_032782 Figure 5262: DNA326578, NM_032377, gen.XM_085909 gen.NM_032377 Figure 5298: DNA269894, NM_002730, Figure 5263: PRO82939 gen.NM_002730 Figure 5264: DNA326579, XM_015697, Figure 5299: PRO58292 gen.XM_015697 Figure 5300: DNA326596, NM_018154, Figure 5265: PRO82940 gen.NM_018154 Figure 5266: DNA326580, XM_010156, Figure 5301: PRO82954 gen.XM_010156 Figure 5302: DNA326597, XM_031276, Figure 5267: DNA326581, NM_001930, gen.XM_031276 gen.NM_001930 Figure 5303: DNA326598, XM_031273, Figure 5268: PRO58446 gen.XM_031273 Figure 5269: DNA326582, NM_013406, Figure 5304: PRO82956 gen.NM_013406 Figure 5305: DNA326599, XM 2031263, Figure 5270: DNA326583, NM_013407, gen.XM_031263 gen.NM_013407 Figure 5306: PRO82957 Figure 5271: PRO82943 Figure 5307: DNA326600, XM_031251, Figure 5272: DNA103320, NM .002229, gen.XM_031251 gen.NM_002229 Figure 5308: DNA326601, NM_006844, Figure 5273: PRO4650 gen.NM_006844 Figure 5274: DNA326584, XM_009063, Figure 5309: PRO82958 gen.XM_009063 Figure 5310A-C: DNA326602, XM_009303, Figure 5275: PRO82944 gen.XM_009303 Figure 5276: DNA326585, XM_085917, Figure 5311: DNA326603, XM_086074, gen.XM_085917 gen.XM_086074 Figure 5277: DNA274034, NM_006397, Figure 5312: DNA269630, NM_003290, gen.NM_006397 gen.NM_003290 Figure 5278: PRO61977 Figure 5313: PRO58042 Figure 5279: DNA287243, NM_004461, Figure 5314: DNA326604, NM_005370, gen.NM_004461 gen.NM_005370

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Figure 5315: PRO12130 Figure 5350: DNA326625, NM_012181. Figure 5316: DNA326605, XM_113348, gen.NM_012181 gen.XM_113348 Figure 5351: PRO82980 Figure 5317: DNA326606, NM_032207, Figure 5352: DNA227249, NM_007263, gen.NM_032207 gen.NM_007263 Figure 5318: PRO82962 Figure 5353: PRO37712 Figure 5319A-B: DNA326607, NM_006387, Figure 5354: DNA326626, XM_018515, gen.NM_006387 gen.XM_018515 Figure 5320: PRO82963 Figure 5355: DNA326627, NM_033415, Figure 5321: DNA326608, NM_024881, gen.NM_033415 gen.NM_024881 Figure 5356: PRO82982 Figure 5322: PRO82964 Figure 5357: DNA326628, XM_009330, Figure 5323: DNA326609, NM_024104, gen.XM_009330 gen.NM_024104 Figure 5358: DNA326629, NM_134440, Figure 5324: PRO82965 gen.NM_134440 Figure 5325A-C: DNA326610, XM _008854, Figure 5359: PRO82983 Figure 5360: DNA326630, NM _003721, gen.XM_008854 Figure 5326: DNA326611, NM_014173, gen.NM_003721 gen.NM_014173 Figure 5361: PRO59220 Figure 5327: PRO82967 Figure 5362: DNA326631, NM_015965, Figure 5328: DNA287240, NM_004335, gen.NM_015965 gen.NM_004335 Figure 5363: PRO82984 Figure 5329: PRO29371 Figure 5364: DNA326632, XM_016378, Figure 5330: DNA326612, XM_050660, gen.XM_016378 gen.XM_050660 Figure 5365: PRO82985 Figure 5331: DNA326613, XM_086116, Figure 5366: DNA326633, XM_114027, gen.XM_086116 gen.XM_114027 Figure 5332: DNA326614, NM_018174, Figure 5367: DNA326634, XM_165963, gen.NM_018174 gen.XM_165963 Figure 5333: PRO82970 Figure 5368: PRO82987 Figure 5334: DNA326615, NM_000980, Figure 5369: DNA326635, XM_015769, gen.NM_000980 gen.XM_015769 Figure 5335: PRO82971 Figure 5370: DNA326636, XM_012812, Figure 5336: DNA326616, XM _055230, gen.XM_012812 Figure 5371: DNA326637, XM_085971, gen.XM_055230 Figure 5337: DNA326617, XM_012179, gen.XM_085971 gen.XM_012179 Figure 5372: DNA326638, XM _037662, Figure 5338A-B: DNA326618, XM_009293, gen.XM_037662 gen.XM_009293 Figure 5373: PRO82991 Figure 5339: DNA326619, XM..038146, Figure 5374: DNA326639, NM_001238, gen.XM_038146 gen.NM_001238 Figure 5340: PRO82975 Figure 5375: PRO82992 Figure 5341: DNA326620, XM_092046, Figure 5376: DNA326640, NM_057182, gen.XM_092046 gen.NM_057182 Figure 5342: PRO82976 Figure 5377: PRO4756 Figure 5343: DNA326621, XM_038098, Figure 5378: DNA326641, XM_009180, gen.XM_038098 gen.XM_009180 Figure 5344: PRO82977 Figure 5379: DNA326642, XM_117118, Figure 5345: DNA326622, NM_032627, gen.XM_117118 gen.NM_032627 Figure 5380: DNA326643, XM_092049, Figure 5346: PRO82978 gen.XM_092049 Figure 5347: DNA326623, XM_165960, Figure 5381: PRO82995 gen.XM_165960 Figure 5382: DNA326644, XM_028672, Figure 5348: PRO82979 gen.XM_028672 Figure 5349: DNA326624, XM_114004, Figure 5383: DNA326645, XM_028666, gen.XM_114004 gen.XM_028666

Figure 5384: DNA326646, XM_009338, gen.XM_059045 gen.XM_009338 Figure 5420: PRO83013 Figure 5385: DNA326647, XM_048258, Figure 5421: DNA273474, NM_005884. gen.XM_048258 gen.NM_005884 Figure 5386: PRO82998 Figure 5422: PRO61458 Figure 5387: DNA256836, NM_018468, Figure 5423: DNA326666, XM_046090, gen.NM_018468 gen.XM_046090 Figure 5388: PRO51767 Figure 5424: PRO83014 Figure 5389: DNA326648, NM_024321, Figure 5425: DNA326667, XM_086004, gen.NM_024321 gen.XM_086004 Figure 5390: PRO82999 Figure 5426: DNA272347, NM _001020, Figure 5391A-B: DNA326649, XM_049237, gen.NM_001020 gen.XM_049237 Figure 5427: PRO60603 Figure 5392: PRO83000 Figure 5428A-B: DNA326668, NM_003169, Figure 5393: DNA326650, NM_032635, gen.NM_003169 gen.NM_032635 Figure 5429: PRO12822 Figure 5394: PRO23845 Figure 5430: DNA326669, XM_053074. Figure 5395: DNA326651, XM_115615, gen.XM_053074 gen.XM_115615 Figure 5431: PRO83016 Figure 5396A-B: DNA326652, XM_091984. Figure 5432: DNA326670, NM_016941. gen.XM_091984 gen.NM_016941 Figure 5397: PRO83002 Figure 5433: PRO83017 Figure 5398: DNA326653, XM_085986. Figure 5434: DNA256840, NM_004714, gen.XM_085986 gen.NM_004714 Figure 5399: DNA326654, XM_032285, Figure 5435: PRO51771 Figure 5436: DNA326671, NM_001436, gen.XM_032285 Figure 5400: PRO83004 gen.NM_001436 Figure 5401: DNA326655, NM_002812, Figure 5437: PRO83018 gen.NM_002812 Figure 5438: DNA326672, XM_016410, Figure 5402: PRO83005 gen.XM_016410 Figure 5403A-E: DNA326656, XM_029455, Figure 5439: DNA326673, XM_012860, gen.XM_029455 gen.XM_012860 Figure 5404: DNA326657, XM_029450, Figure 5440: DNA326674, XM_097365, gen.XM_029450 gen.XM_097365 Figure 5405: PRO83007 Figure 5441: DNA274139, NM_006503, Figure 5406: DNA326658, XM _009149, gen.NM_006503 gen.XM_009149 Figure 5442: PRO62075 Figure 5407: PRO62500 Figure 5443: DNA326675, XM_009203, Figure 5408: DNA326659, XM_056602, gen.XM_009203 gen.XM_056602 Figure 5444: DNA326676, XM_047409, Figure 5409: DNA326660, NM_012237, gen.XM_047409 gen.NM_012237 Figure 5445: DNA326677, XM_047376, Figure 5410: PRO83008 gen.XM_047376 Figure 5411: DNA326661, NM_030593, Figure 5446A-B: DNA326678, XM_047374, gen.NM_030593 gen.XM_047374 Figure 5412: PRO83009 Figure 5447: DNA326679, XM_059052. Figure 5413: DNA326662, NM_017827, gen.XM_059052 gen.NM_017827 Figure 5448: DNA273600, NM_004596, Figure 5414: PRO83010 gen.NM_004596 Figure 5415: DNA326663, NM_021107, Figure 5449: PRO61575 gen.NM_021107 Figure 5450: DNA326680, XM_030914, Figure 5416: PRO83011 gen.XM_030914 Figure 5417: DNA326664, NM_033363, Figure 5451: DNA326681, NM_052848, gen.NM_033363 gen.NM_052848 Figure 5418: PRO83012 Figure 5452: PRO83027 Figure 5419: DNA326665, XM_059045, Figure 5453: DNA326682, XM_008912,

gen.XM_008912 gen.XM_085950 Figure 5454: DNA326683, NM_020158, Figure 5488: DNA326704, XM_028263, gen.NM_020158 gen.XM_028263 Figure 5455: PRO83029 Figure 5489: DNA326705, XM_085928, Figure 5456: DNA326684, XM_030901, gen.XM_085928 gen.XM_030901 Figure 5490: PRO36963 Figure 5457: PRO83030 Figure 5491: DNA326706, XM _028267, Figure 5458: DNA326685, NM_018035, gen.XM_028267 gen.NM_018035 Figure 5492: DNA326707, NM_013403, Figure 5459: PRO83031 gen.NM_013403 Figure 5460: DNA326686, XM _085874, Figure 5493: PRO83050 gen.XM_085874 Figure 5494: DNA103580, NM_001743, Figure 5461: DNA326687, XM_085875, gen.NM_001743 gen.XM_085875 Figure 5495: PRO4904 Figure 5462: DNA326688, XM_085876, Figure 5496: DNA326708, XM_009126, gen.XM_085876 gen.XM_009126 Figure 5497: DNA326709, NM_006247, Figure 5463: DNA326689, XM_058949, gen.XM_058949 gen.NM_006247 Figure 5464: PRO83035 Figure 5498: PRO25881 Figure 5465: DNA326690, XM_030895, Figure 5499: DNA326710, NM_003370, gen.XM_030895 gen.NM_003370 Figure 5466: DNA326691, XM_115603, Figure 5500: PRO83052 gen.XM_115603 Figure 5501: DNA326711, XM_085856, Figure 5467: PRO83037 gen.XM_085856 Figure 5468: DNA326692, NM_001022, Figure 5502: DNA150784, NM_001983, gen.NM_001022 gen.NM_001983 Figure 5469: PRO83038 Figure 5503: PRO12800 Figure 5470: DNA326693, NM_004706, Figure 5504: DNA270931, NM_012099, gen.NM_004706 gen.NM_012099 Figure 5471: PRO83039 Figure 5505: PRO59264 Figure 5472: DNA326694, XM_008878, Figure 5506A-B: DNA257531, NM_031417, gen.XM_008878 gen.NM_031417 Figure 5473: PRO83040 Figure 5507: PRO52101 Figure 5474: DNA326695, NM_022752, Figure 5508: DNA326712, NM_001294, gen.NM_022752 gen.NM_001294 Figure 5475: PRO83041 Figure 5509: PRO83054 Figure 5476: DNA151808, NM_006494, Figure 5510: DNA326713, XM_097274, gen.NM_006494 gen.XM_097274 Figure 5477: PRO12892 Figure 5511: DNA88084, NM _000041, Figure 5478: DNA326696, NM_001816, gen.NM_000041 gen.NM_001816 Figure 5512: PRO2644 Figure 5479: PRO34151 Figure 5513: DNA256533, NM_006114, gen.NM_006114 Figure 5480: DNA326697, NM_000554, gen.NM_000554 Figure 5514: PRO51565 Figure 5515: DNA251057, NM_002856, Figure 5481: PRO83042 Figure 5482: DNA326698, XM_049920, gen.NM_002856 gen.XM_049920 Figure 5516: PRO47354 Figure 5483: DNA326699, XM_055859, Figure 5517: DNA226011, NM_005581, gen.XM_055859 gen.NM_005581 Figure 5484A-B: DNA326700, XM_009125, Figure 5518: PRO36474 Figure 5519: DNA326714, NM_012116, gen.XM_009125 Figure 5485: DNA326701, XM_008860, gen.NM_012116 gen.XM_008860 Figure 5520: PRO83056 Figure 5486: DNA326702, XM_009036, Figure 5521: DNA326715, XM_097275, gen.XM_009036 gen.XM_097275 Figure 5487: DNA326703, XM_085950, Figure 5522: DNA326716, XM_008851,

gen.XM_008851 gen.NM_003598 Figure 5523: DNA274289, NM_016440. Figure 5557: PRO83075 gen.NM_016440 Figure 5558: DNA326736, NM_006666, Figure 5524: PRO62212 gen.NM_006666 Figure 5525: DNA326717, NM_012068, Figure 5559: PRO83076 gen.NM_012068 Figure 5560: DNA326737, XM_114024, Figure 5526: PRO83059 gen.XM_114024 Figure 5527: DNA326718, XM_085927, Figure 5561: PRO83077 gen.XM_085927 Figure 5562: DNA304658, NM_000146, Figure 5528: DNA326719, XM_084023. gen.NM_000146 gen.XM_084023 Figure 5563: PRO71085 Figure 5529: DNA326720, XM_167530, Figure 5564: DNA326738, NM_004324, gen.XM_167530 gen.NM_004324 Figure 5530: DNA326721, XM_114025. Figure 5565: PRO38101 gen.XM_114025 Figure 5566: DNA326739, NM_006184, Figure 5531: DNA326722, XM_008985. gen.NM_006184 gen.XM_008985 Figure 5567: PRO83078 Figure 5532: DNA326723, NM_030973, Figure 5568: DNA273066, NM_001190. gen.NM_030973 gen.NM_001190 Figure 5533: PRO83065 Figure 5569: PRO61129 Figure 5534: DNA326724, NM_025129, Figure 5570: DNA326740, XM_058987, gen.NM_025129 gen.XM_058987 Figure 5535: PRO83066 Figure 5571: DNA326741, NM _000979, Figure 5536: DNA326725, NM_014203, gen.NM_000979 gen.NM_014203 Figure 5572: PRO83080 Figure 5537: DNA326726, XM_085934, Figure 5573: DNA326742, XM_085935, gen.XM_085934 gen.XM_085935 Figure 5538: PRO83068 Figure 5574: DNA326743, NM_031485, Figure 5539: DNA326727, NM_001536, gen.NM_031485 gen.NM_001536 Figure 5575: PRO61308 Figure 5540: PRO83069 Figure 5576: DNA103239, NM_006801, Figure 5541: DNA326728, XM_165432, gen.NM_006801 gen.XM_165432 Figure 5577: PRO4569 Figure 5542: DNA274823, NM_001571, Figure 5578: DNA326744, XM_046419, gen.NM_001571 gen.XM_046419 Figure 5543: PRO62582 Figure 5579: PRO83082 Figure 5544A-B: DNA326729, XM_046313, Figure 5580: DNA326745, NM_002691, gen.XM_046313 gen.NM_002691 Figure 5545: PRO83071 Figure 5581: PRO83083 Figure 5546: DNA326730, NM_015953, Figure 5582: DNA326746, XM_056286, gen.NM_015953 gen.XM_056286 Figure 5547: PRO83072 Figure 5583: PRO83084 Figure 5548: DNA326731, XM_027904. Figure 5584: DNA326747, XM_058990, gen.XM_027904 gen.XM_058990 Figure 5549: DNA326732, XM_084026, Figure 5585: PRO83085 gen.XM_084026 Figure 5586: DNA326748, XM_091981, Figure 5550: DNA290260, NM_012423, gen.XM_091981 gen.NM_012423 Figure 5587: PRO83086 Figure 5551: PRO70385 Figure 5588: DNA326749, NM_032712, Figure 5552: DNA326733, XM_058991, gen.NM_032712 gen.XM_058991 Figure 5589: PRO23238 Figure 5553: PRO83073 Figure 5590: DNA83154, NM_001648, Figure 5554: DNA326734, NM_017916, gen.NM_001648 gen.NM_017916 Figure 5591: PRO2109 Figure 5555: PRO83074 Figure 5592: DNA326750, XM_055658, Figure 5556: DNA326735, NM_003598, gen.XM_055658

Figure 5593: DNA269481, NM_001985, gen.NM_001985 Figure 5594: PRO57901 Figure 5595: DNA326751, XM_091886, gen.XM_091886 Figure 5596: PRO83087 Figure 5597: DNA326752, XM_008830, gen.XM_008830 Figure 5598: DNA326753, XM_039908, gen.XM_039908 Figure 5599: PRO83089 Figure 5600: DNA326754, NM_015629, gen.NM_015629 Figure 5601: PRO83090 Figure 5602: DNA326755, XM_050236, gen.XM_050236 Figure 5603: DNA326756, XM_050589. gen.XM_050589 Figure 5604: PRO83092 Figure 5605: DNA326757, XM_117128, gen.XM_117128 Figure 5606: PRO83093 Figure 5607: DNA326758, XM_059321, gen.XM_059321 Figure 5608: DNA326759, NM_003283, gen.NM_003283 Figure 5609: PRO83095 Figure 5610A-B: DNA326760, NM_014931, gen.NM_014931 Figure 5611: PRO83096 Figure 5612: DNA326761, XM _035919, gen.XM_035919 Figure 5613: DNA326762, NM_000991, gen.NM_000991 Figure 5614: PRO83098 Figure 5615: DNA273346, NM_014501, gen.NM_014501 Figure 5616: PRO61349 Figure 5617: DNA326763, NM_013333, gen.NM_013333 Figure 5618: PRO83099 Figure 5619: DNA326764, NM_007279, gen.NM_007279 Figure 5620: PRO83100 Figure 5621: DNA326765, NM_016202, gen.NM_016202 Figure 5622: PRO83101 Figure 5623: DNA326766, XM_034377, gen.XM_034377 Figure 5624: PRO83102 Figure 5625: DNA272062, NM_014453, gen.NM_014453 Figure 5626: PRO60333 Figure 5627: DNA254548, NM_005762,

Figure 5629: DNA326767, XM_085972, gen.XM_085972 Figure 5630: PRO83103 Figure 5631: DNA326768, NM_032792, gen.NM_032792 Figure 5632: PRO83104 Figure 5633: DNA326769, NM_001009, gen.NM_001009 Figure 5634: PRO83105 Figure 5635: DNA326770, XM_058125, gen.XM_058125 Figure 5636: DNA326771, NM _024691, gen.NM_024691 Figure 5637: PRO83107 Figure 5638: DNA297288, NM_021158, gen.NM_021158 Figure 5639: PRO70810 Figure 5640: DNA304662, NM_031229, gen.NM_031229 Figure 5641: PRO71089 Figure 5642: DNA326772, NM_031228, gen.NM_031228 Figure 5643: PRO83108 Figure 5644: DNA326773, XM_097749, gen.XM_097749 Figure 5645: PRO83109 Figure 5646: DNA326774, XM_055993, gen.XM_055993 Figure 5647: DNA326775, XM_009622, gen.XM_009622 Figure 5648: DNA326776, NM_000801, gen.NM_000801 Figure 5649: PRO59142 Figure 5650: DNA326777, NM_054014, gen.NM_054014 Figure 5651: PRO59142 Figure 5652: DNA326778, NM_016143, gen.NM_016143 Figure 5653: PRO83112 Figure 5654: DNA287270, NM_003091, gen.NM_003091 Figure 5655: PRO69541 Figure 5656: DNA326779, NM_052881, gen.NM_052881 Figure 5657: PRO83113 Figure 5658: DNA326780, XM_044914, gen.XM_044914 Figure 5659: PRO83114 Figure 5660: DNA326781, XM_044915, gen.XM_044915 Figure 5661: DNA326782, NM .006899, gen.NM_006899 Figure 5662: PRO83116 Figure 5663: DNA326783, NM_019609, gen.NM_019609 Figure 5664: PRO83117

gen.NM_005762

Figure 5628: PRO49653

Figure 5665: DNA326784, NM_021826, Figure 5699: PRO83133 gen.NM_021826 Figure 5700: DNA326801, XM_012970, Figure 5666: PRO83118 gen.XM_012970 Figure 5667: DNA326785, XM_045418, Figure 5701: DNA326802, XM _042765, gen.XM_045418 gen.XM_042765 Figure 5668: DNA287261, NM_017874. Figure 5702: PRO83135 gen.NM_017874 Figure 5703: DNA150548, NM_001247, Figure 5669: PRO69533 gen.NM_001247 Figure 5670: DNA326786, XM_086710, Figure 5704: PRO12324 gen.XM_086710 Figure 5705A-B: DNA326803, XM_009436, Figure 5671: DNA326787, XM_045451. gen.XM_009436 gen.XM_045451 Figure 5706: DNA326804, XM_114178, Figure 5672: PRO83121 gen.XM_114178 Figure 5673: DNA326788, XM_114174, Figure 5707: PRO83137 gen.XM_114174 Figure 5708: DNA326805, XM_046160, Figure 5674: DNA326789, XM_045460. gen.XM_046160 gen.XM_045460 Figure 5709: PRO83138 Figure 5675: DNA326790, XM_059268. Figure 5710: DNA326806, XM_046179, gen.XM_059268 gen.XM_046179 Figure 5676A-B: DNA271010, NM_014737, Figure 5711: PRO83139 gen.NM_014737 Figure 5712: DNA326807, XM_086745, Figure 5677: PRO59339 gen.XM_086745 Figure 5678: DNA326791, XM_056035, Figure 5713: DNA326808, NM_138578, gen.XM_056035 gen.NM_138578 Figure 5679: DNA83170, NM_001819, Figure 5714: PRO83141 gen.NM_001819 Figure 5715: DNA326809, NM_012112, Figure 5680: PRO2615 gen.NM_012112 Figure 5681: DNA227348, NM_019095, Figure 5716: PRO83142 gen.NM_019095 Figure 5717: DNA326810, XM_086736, Figure 5682: PRO37811 gen.XM_086736 Figure 5683: DNA326792, NM _003092, Figure 5718: PRO83143 gen.NM_003092 Figure 5719: DNA326811, NM_030815, Figure 5684: PRO83125 gen.NM_030815 Figure 5685: DNA287290, NM_014426, Figure 5720: PRO83144 gen.NM_014426 Figure 5721A-B: DNA150767, NM_014742, Figure 5686: PRO69560 gen.NM_014742 Figure 5687: DNA326793, XM_086701. Figure 5722: PRO12460 gen.XM_086701 Figure 5723A-B: DNA326812, XM_047007, Figure 5688: DNA326794, XM_117209, gen.XM_047007 gen.XM_117209 Figure 5724: PRO83145 Figure 5689A-B: DNA326795, XM_046520, Figure 5725A-B: DNA326813, XM_047011, gen.XM_046520 gen.XM_047011 Figure 5690: PRO83128 Figure 5726: PRO83146 Figure 5691: DNA326796, XM_115846, Figure 5727A-B: DNA326814, XM_047018, gen.XM_115846 gen.XM_047018 Figure 5692: PRO83129 Figure 5728: DNA326815, XM_009450, Figure 5693: DNA326797, NM_080820, gen.XM_009450 gen.NM_080820 Figure 5729: DNA326816, NM_033197, Figure 5694: PRO83130 gen.NM_033197 Figure 5695: DNA326798, XM_086715, Figure 5730: PRO83149 gen.XM_086715 Figure 5731: DNA326817, XM_097772, Figure 5696: DNA326799, XM_092760, gen.XM_097772 gen.XM_092760 Figure 5732: PRO83150 Figure 5697: PRO83132 Figure 5733: DNA326818, NM_016732, Figure 5698: DNA326800, NM_012255, gen.NM_016732 gen.NM_012255 Figure 5734: DNA97298, NM_003908,

gen.NM_003908 gen.NM_024855 Figure 5735: PRO3645 Figure 5770: PRO83165 Figure 5736: DNA326819, NM_000687. Figure 5771A-B: DNA227472, NM_002660, gen.NM_000687 gen.NM_002660 Figure 5737: PRO83152 Figure 5772: PRO37935 Figure 5738: DNA273517, NM_000178, Figure 5773: DNA326836, XM_097727, gen.NM_000178 gen.XM_097727 Figure 5739: PRO61498 Figure 5774: DNA103525, NM_002466, Figure 5740: DNA326820, NM_018217, gen.NM_002466 gen.NM_018217 Figure 5775: PRO4852 Figure 5741: PRO83153 Figure 5776: DNA326837, XM_029810, Figure 5742: DNA326821, NM_002212, gen.XM_029810 gen.NM_002212 Figure 5777: PRO83167 Figure 5743: PRO60945 Figure 5778: DNA326838, XM_029822, Figure 5744A-C: DNA326822, NM_007186, gen.XM_029822 gen.NM_007186 Figure 5779: DNA326839, NM_002638, Figure 5745: DNA226758, NM_015966, gen.NM_002638 gen.NM_015966 Figure 5780: PRO2065 Figure 5746: PRO37221 Figure 5781: DNA326840, NM _003064, Figure 5747: DNA194701, NM_003915, gen.NM_003064 gen.NM_003915 Figure 5782: PRO1720 Figure 5748: PRO24002 Figure 5783: DNA326841, NM_015937, Figure 5749: DNA326823, XM_113380, gen.NM_015937 gen.XM_113380 Figure 5784: PRO83169 Figure 5750: DNA326824, NM_016558. Figure 5785: DNA273320, NM_007019, gen.NM_016558 gen.NM_007019 Figure 5751: PRO83155 Figure 5786: PRO61327 Figure 5752: DNA326825, NM_015511, Figure 5787: DNA326842, NM_033421, gen.NM_015511 gen.NM_033421 Figure 5753: PRO83156 Figure 5788: PRO83170 Figure 5754: DNA326826, XM_009501, Figure 5789: DNA88569, NM_006227, gen.XM_009501 gen.NM_006227 Figure 5755: PRO83157 Figure 5790: PRO2420 Figure 5756: DNA326827, XM_057236, Figure 5791: DNA88239, NM_004994, gen.XM_057236 gen.NM_004994 Figure 5757: DNA326828, NM_024918, Figure 5792: PRO2711 Figure 5793: DNA326843, XM_057374, gen.NM_024918 Figure 5758: PRO83159 gen.XM_057374 Figure 5759: DNA326829, XM_009642, Figure 5794: DNA326844, XM_114163, gen.XM_009642 gen.XM_114163 Figure 5760: DNA194807, NM_006698. Figure 5795A-B: DNA326845, XM_097731, gen.NM_006698 gen.XM_097731 Figure 5761: PRO24077 Figure 5796A-B: DNA326846, XM_030044, Figure 5762: DNA326830, XM_009686, gen.XM_030044 gen.XM_009686 Figure 5797: PRO83174 Figure 5763: DNA326831, NM_030877, Figure 5798: DNA326847, NM_017895, gen.NM_030877 gen.NM_017895 Figure 5764: PRO83161 Figure 5799: PRO83175 Figure 5800: DNA326848, XM_097713, Figure 5765: DNA326832, XM_028806, gen.XM_028806 gen.XM_097713 Figure 5766A-B: DNA326833, XM_028810, Figure 5801: PRO83176 Figure 5802: DNA326849, NM_005985, gen.XM_028810 Figure 5767: PRO83163 gen.NM_005985 Figure 5768: DNA326834, XM_012931, Figure 5803: PRO83177 gen.XM_012931 Figure 5804: DNA326850, NM_003349, Figure 5769: DNA326835, NM_024855, gen.NM_003349

Figure 5805: PRO83178 Figure 5841: PRO83190 Figure 5806: DNA326851, NM_022442, Figure 5842: DNA326868, XM_037206, gen.NM_022442 gen.XM_037206 Figure 5807: PRO83179 Figure 5843: PRO83191 Figure 5808: DNA326852, NM_005194, Figure 5844: DNA 103486, NM _007002, gen.NM_005194 gen.NM_007002 Figure 5809: DNA326853, NM_002827, Figure 5845: PRO4813 gen.NM_002827 Figure 5846A-D: DNA326869, XM_037217. Figure 5810: PRO38066 gen.XM_037217 Figure 5811: DNA326854, NM_003859. Figure 5847: DNA326870, NM_001024, gen.NM_003859 gen.NM_001024 Figure 5812: PRO83180 Figure 5848: PRO83193 Figure 5813: DNA326855, XM_114165, Figure 5849: DNA326871, NM_018270, gen.XM_114165 gen.NM_018270 Figure 5814: DNA269526, NM_001324, Figure 5850: PRO83194 gen.NM_001324 Figure 5851: DNA326872, XM_028783, Figure 5815: PRO57942 gen.XM_028783 Figure 5816: DNA326856, XM_009549, Figure 5852: PRO83195 gen.XM_009549 Figure 5853: DNA326873, NM_001853, Figure 5817: PRO83182 gen.NM_001853 Figure 5818: DNA326857, XM_030621, Figure 5854: PRO83196 gen.XM_030621 Figure 5855: DNA326874, NM_080796, Figure 5819: DNA326858, XM_086648. gen.NM_080796 gen.XM_086648 Figure 5856: PRO83197 Figure 5820: PRO83183 Figure 5857: DNA326875, NM_022105, Figure 5821: DNA326859, XM_009672, gen.NM_022105 gen.XM_009672 Figure 5858: PRO83198 Figure 5822: PRO83184 Figure 5859: DNA326876, NM_080797, Figure 5823A-B: DNA326860, XM_009671, gen.NM_080797 gen.XM_009671 Figure 5860: PRO83199 Figure 5824: DNA326861, NM_004738, Figure 5861: DNA326877, NM_018209, gen.NM_004738 gen.NM_018209 Figure 5825: PRO983 Figure 5862: PRO83200 Figure 5826: DNA326862, NM_016592, Figure 5863A-C: DNA326878, XM_028834, gen.NM_016592 gen.XM_028834 Figure 5827: PRO83185 Figure 5864: PRO83201 Figure 5828: DNA326863, NM_080425, Figure 5865: DNA326879, NM_024299, gen.NM_080425 gen.NM_024299 Figure 5829: PRO83186 Figure 5866: PRO83202 Figure 5830: DNA304670, NM_000516. Figure 5867A-C: DNA326880, XM_028918, gen.NM_000516 gen.XM_028918 Figure 5831: PRO71097 Figure 5868: PRO83203 Figure 5832: DNA326864, NM_080426, Figure 5869: DNA326881, NM_032527, gen.NM_080426 gen.NM_032527 Figure 5833: PRO83187 Figure 5870: PRO83204 Figure 5834: DNA326865, XM_030699, Figure 5871A-B: DNA326882, XM_028966, gen.XM_030699 gen.XM_028966 Figure 5835: PRO83188 Figure 5872: PRO83205 Figure 5836: DNA188229, NM_000114. Figure 5873: DNA269746, NM_012469, gen.NM_000114 gen.NM_012469 Figure 5837: PRO21728 Figure 5874: PRO58155 Figure 5838: DNA326866, NM_002792, Figure 5875: DNA326883, XM_114154, gen.NM_002792 gen.XM_114154 Figure 5839: PRO83189 Figure 5876: DNA326884, XM_072173, Figure 5840A-B: DNA326867, XM_037202, gen.XM_072173 gen.XM_037202 Figure 5877: DNA326885, XM_086759,

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gen.XM_086759 Figure 5913: DNA326901, XM_036042, Figure 5878: DNA326886, XM_086760, gen.XM_036042 gen.XM_086760 Figure 5914: DNA326902, XM_086770, Figure 5879: DNA326887, NM_021219, gen.XM_086770 gen.NM_021219 Figure 5915: DNA326903, NM .004928, Figure 5880: PRO28687 gen.NM_004928 Figure 5881: DNA188732, NM_000484, Figure 5916: PRO83222 gen.NM_000484 Figure 5917: DNA326904, XM _036087, Figure 5882: PRO25302 gen.XM_036087 Figure 5883: DNA326888, NM_016940, Figure 5918: PRO83223 gen.NM_016940 Figure 5919: DNA326905, XM_009805, Figure 5884: PRO83210 gen.XM_009805 Figure 5885: DNA254572, NM_006585, Figure 5920: PRO83224 gen.NM_006585 Figure 5921: DNA226409, NM_004339, Figure 5886: PRO49675 gen.NM_004339 Figure 5887: DNA326889, NM_005806, Figure 5922: PRO36872 gen.NM_005806 Figure 5923: DNA326906, XM_036107, Figure 5888: PRO83211 gen.XM_036107 Figure 5889: DNA326890, XM_114185, Figure 5924A-B: DNA326907, XM_036175, gen.XM_114185 gen.XM_036175 Figure 5890: DNA254994, NM_017613. Figure 5925: DNA326908, XM _097817, gen.NM_017613 gen.XM_097817 Figure 5891: PRO50083 Figure 5926A-B: DNA326909, XM_054566, Figure 5892: DNA274129, NM_001697, gen.XM_054566 Figure 5927: DNA326910, XM_036755, gen.NM_001697 Figure 5893: PRO62065 gen.XM_036755 Figure 5894: DNA326891, NM_001757, Figure 5928: DNA326911, XM_086773, gen.NM_001757 gen.XM_086773 Figure 5929: DNA326912, XM_097807, Figure 5895: PRO83212 Figure 5896A-C: DNA151898, NM_003316, gen.XM_097807 gen.NM_003316 Figure 5930: DNA326913, XM_086777, Figure 5897: PRO12135 gen.XM_086777 Figure 5898: DNA326892, NM_003720, Figure 5931: DNA326914, NM_002340, gen.NM_003720 gen.NM_002340 Figure 5899: PRO83213 Figure 5932: PRO83233 Figure 5900: DNA326893, NM_002606, Figure 5933A-B: DNA326915, NM_003906, gen.NM_003906 gen.NM_002606 Figure 5901: PRO83214 Figure 5934: PRO83234 Figure 5902: DNA326894, XM_033015, Figure 5935: DNA226617, NM_006272, gen.NM_006272 gen.XM_033015 Figure 5936: PRO37080 Figure 5903: DNA326895, XM_033016, Figure 5937: DNA326916, NM_033070, gen.XM_033016 Figure 5904: PRO59669 gen.NM_033070 Figure 5905: DNA326896, NM_003681, Figure 5938: PRO83235 gen.NM_003681 Figure 5939: DNA255046, NM_017829, gen.NM_017829 Figure 5906: PRO69486 Figure 5940: PRO50134 Figure 5907: DNA326897, XM_035999, gen.XM_035999 Figure 5941: DNA326917, NM_001696, Figure 5908: DNA326898, NM_020132, gen.NM_001696 Figure 5942: PRO83236 gen.NM_020132 Figure 5943A-B: DNA326918, XM_032996, Figure 5909: PRO83217 Figure 5910: DNA326899, XM_036011, gen.XM_032996 Figure 5944: PRO83237 gen.XM_036011 Figure 5945: DNA326919, XM_167538, Figure 5911: DNA326900, NM_013369, gen.NM_013369 gen.XM_167538 Figure 5946: DNA326920, XM_033090, Figure 5912: PRO83219

gen.XM_033090 Figure 5981A-B: DNA326938, XM_037797, Figure 5947: DNA225954, NM_000407, gen.XM_037797 gen.NM_000407 Figure 5982: PRO83256 Figure 5948: PRO36417 Figure 5983: DNA326939, NM_004175, Figure 5949: DNA326921, XM_058918, gen.NM_004175 gen.XM_058918 Figure 5984: PRO83257 Figure 5950: DNA326922, XM_097833, Figure 5985: DNA326940, XM_086821, gen.XM_097833 gen.XM_086821 Figure 5951: DNA326923, NM_024627, Figure 5986: DNA326941, XM_092888, gen.NM_024627 gen.XM_092888 Figure 5952: PRO83242 Figure 5987: DNA326942, NM _005080, Figure 5953: DNA326924, XM_086809, gen.NM_005080 gen.XM_086809 Figure 5988: PRO83260 Figure 5954: DNA326925, NM_006440, Figure 5989: DNA269830, NM_005243, gen.NM_006440 gen.NM_005243 Figure 5955: PRO83244 Figure 5990: PRO58232 Figure 5956: DNA226561, NM_000754, Figure 5991: DNA326943, NM_006478, gen.NM_000754 gen.NM_006478 Figure 5957: PRO37024 Figure 5992: PRO83261 Figure 5958: DNA326926, NM_007310. Figure 5993A-B: DNA326944, XM_037945, gen.NM_007310 gen.XM_037945 Figure 5959: PRO83245 Figure 5994: DNA103462, NM_000268, Figure 5960A-B: DNA326927, XM_033813, gen.NM_000268 gen.XM_033813 Figure 5995: PRO4789 Figure 5961: DNA326928, NM_022727, Figure 5996: DNA326945, NM_032204, gen.NM_022727 gen.NM_032204 Figure 5962: PRO83247 Figure 5997: PRO83263 Figure 5963: DNA326929, XM_086805, Figure 5998: DNA326946, XM_066291, gen.XM_086805 gen.XM_066291 Figure 5964: DNA326930, XM_086873, Figure 5999: DNA326947, NM_005877, gen.XM_086873 gen.NM_005877 Figure 5965: DNA257549, NM_030573, Figure 6000: PRO62328 gen.NM_030573 Figure 6001: DNA326948, NM_016498, Figure 5966: PRO52119 gen.NM_016498 Figure 5967: DNA326931, XM_096155, Figure 6002: PRO83265 gen.XM_096155 Figure 6003: DNA254141, NM_014303, Figure 5968: DNA326932, XM .096156, gen.NM_014303 gen.XM_096156 Figure 6004: PRO49256 Figure 5969A-B: DNA326933, XM_036937, Figure 6005A-B: DNA151882, NM_014941, gen.XM_036937 gen.NM_014941 Figure 5970: PRO83252 Figure 6006: PRO12134 Figure 5971: DNA326934, XM_097886, Figure 6007: DNA326949, NM_006932, gen.XM_097886 gen.NM_006932 Figure 5972: PRO83253 Figure 6008: PRO83266 Figure 5973: DNA304835, NM_022044, Figure 6009: DNA326950, NM_134269, gen.NM_022044 gen.NM_134269 Figure 5974: PRO71242 Figure 6010: PRO83267 Figure 5975: DNA326935, NM_006115, Figure 6011: DNA270697, NM_004147, gen.NM_006115 gen.NM_004147 Figure 5976: PRO37012 Figure 6012: PRO59061 Figure 5977: DNA326936, XM_037682, Figure 6013: DNA326951, XM_059335, gen.XM_037682 gen.XM_059335 Figure 5978: PRO83254 Figure 6014: DNA326952, XM_018539, Figure 5979: DNA326937, NM_002415, gen.XM_018539 gen.NM_002415 Figure 6015: DNA326953, NM_014306, Figure 5980: PRO83255 gen.NM_014306

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Figure 6016: PRO83270 Figure 6052: DNA326969, NM_012323. Figure 6017: DNA326954, NM_012179, gen.NM_012323 gen.NM_012179 Figure 6053: PRO83282 Figure 6018: PRO83271 Figure 6054: DNA326970, NM _012264, Figure 6019A-B: DNA326955, XM_038584, gen.NM_012264 gen.XM_038584 Figure 6055: PRO12490 Figure 6020: DNA151752, NM_002133, Figure 6056: DNA326971, NM_015373. gen.NM_002133 gen.NM_015373 Figure 6021: PRO12886 Figure 6057: PRO83283 Figure 6022: DNA326956, XM _009947, Figure 6058: DNA326972, NM_020243, gen.XM_009947 gen.NM_020243 Figure 6023: PRO12845 Figure 6059: PRO23231 Figure 6024: DNA326957, XM_114209, Figure 6060: DNA326973, XM_039339, gen.XM_114209 gen.XM_039339 Figure 6025A-B: DNA326958, NM_002473, Figure 6061: DNA326974, NM _000967, gen.NM_002473 gen.NM_000967 Figure 6026: PRO83273 Figure 6062: PRO83285 Figure 6027: DNA188740, NM_003753. Figure 6063: DNA326975, XM_010000, gen.NM_003753 gen.XM_010000 Figure 6028: PRO22481 Figure 6064: DNA326976, XM_010002, Figure 6029: DNA326959, NM_021126, gen.XM_010002 gen.NM_021126 Figure 6065: DNA326977, XM_039372, Figure 6030: PRO70331 gen.XM_039372 Figure 6031: DNA326960, XM_009967, Figure 6066: DNA326978, XM_013010, gen.XM_009967 gen.XM_013010 Figure 6032: DNA326961, NM_013365, Figure 6067: PRO83288 gen.NM_013365 Figure 6068: DNA254165, NM_000026, Figure 6033: PRO83274 gen.NM_000026 Figure 6034: DNA290259, NM_018957, Figure 6069: PRO49278 gen.NM_018957 Figure 6070: DNA326979, NM_003932, Figure 6035: PRO70383 gen.NM_003932 Figure 6036: DNA326962, NM_020315, Figure 6071: PRO4586 gen.NM_020315 Figure 6072: DNA326980, NM_014248, Figure 6037: PRO83275 gen.NM_014248 Figure 6038: DNA304719, NM_002305, Figure 6073: PRO83289 Figure 6074: DNA326981, XM_086844, gen.NM_002305 Figure 6039: PRO71145 gen.XM_086844 Figure 6040: DNA326963, NM_007032, Figure 6075: DNA219225, NM _002883, gen.NM_007032 gen.NM_002883 Figure 6041: PRO83276 Figure 6076: PRO34531 Figure 6042: DNA326964, XM_009973, Figure 6077: DNA326982, NM_003216, gen.XM_009973 gen.NM_003216 Figure 6043: DNA326965, XM_086830, Figure 6078: PRO83291 Figure 6079: DNA270954, NM _001098, gen.XM_086830 Figure 6044: PRO83278 gen.NM_001098 Figure 6045: DNA254240, NM_016091, Figure 6080: PRO59285 gen.NM_016091 Figure 6081: DNA326983, NM_001469, Figure 6046: PRO49352 gen.NM_001469 Figure 6047A-B: DNA326966, XM_039236, Figure 6082: PRO4872 gen.XM_039236 Figure 6083: DNA326984, NM_005008, Figure 6048: PRO83279 gen.NM_005008 Figure 6049: DNA326967, NM_006941, Figure 6084: PRO83292 gen.NM_006941 Figure 6085A-B: DNA326985, NM_004599, Figure 6050: PRO83280 gen.NM_004599 Figure 6051: DNA326968, XM_039248, Figure 6086: PRO83293

Figure 6087A-B: DNA326986, XM_010024,

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gen.NM_006470,4725	gen.NM_006854,2184
gen.NM_006478,5991	gen.NM_006862,344
gen.NM_006488,703	gen.NM_006888,4063
gen.NM_006494,5476	gen.NM_006899,5661
gen.NM_006503,5441	gen.NM_006908,2182
gen.NM_006513,298	gen.NM_006924,4908
gen.NM_006516,188	gen.NM_006928,3660
gen.NM_006523,3055	gen.NM_006932,6007
gen.NM_006530,3727	gen.NM_006938,5039
gen.NM_006556,452	gen.NM_006941,6049
gen.NM_006559, 146	gen.NM_006942,4691
gen.NM_006576,3697	gen.NM_006990,124
gen.NM_006585,5885	gen.NM_007002,5844
gen.NM_006586, 1894	gen.NM_007002,3844 gen.NM_007019,5785
gen.NM_006589,428	gen.NM_007019,3783 gen.NM_007032,6040
gen.NM_006600,118	gen.NM_007032,0040
gen.NM_006601,3636	gen.NM_007034,207
gen.NM_006621,300	
gen.NM_006625,93	gen.NM_007047,2029 gen.NM_007062,3805
gen.NM_006636,794	gen.NM_007065,5237
gen.NM_006646,3881	<u> </u>
gen.NM_006659,3101	gen.NM_007074,4516 gen.NM_007085,1216
gen.NM_006666,5558	gen.NM_007085,1216 gen.NM_007096,2691
gen.NM_006667,6272	
gen.NM_006670,2070	gen.NM_007100,1366
gen.NM_006693,2344	gen.NM_007103,3299 gen.NM_007104,1922
gen.NM_006694,436	gen.NM_007158,302
gen.NM_006698,5760	-
gen.NM_006708, 1904	gen.NM_007165,5152 gen.NM_007173,3348
gen.NM_006711,4392	gen.NM_007178,3501
gen.NM_006746,6134	gen.NM_007178,3301
gen.NM_006761,4642	gen.NM_007186,5744
gen.NM_006763,548	gen.NM_007190,3089
gen.NM_006764,1151	gen.NM_007209,2794
gen.NM_006769,271	gen.NM_007242,4566
gen.NM_006787,6197	gen.NM_007242,4500
gen.NM_006791,4279	gen.NM_007260,89
gen.NM_006799,4408	gen.NM_007262,42
gen.NM_006801,5576	gen.NM_007263,5352
gen.NM_006805, 1687	gen.NM_007268,6204
gen.NM_006808,2740	gen.NM_007273,3455
gen.NM_006810,1223	gen.NM_007275,1153
gen.NM_006812,3678	gen.NM_007276,2214
gen.NM_006815,3847	gen.NM_007279,5619
gen.NM_006816, 1830	gen.NM_007279,5019 gen.NM_007310,5958
gen.NM_006817,3785	-
gen.NM_006821,4046	gen.NM_007311,6095
gen.NM_006824, 192	gen.NM_007317,4507
gen.NM_006825,3807	gen.NM_007355,1874
gen.NM_006826,655	gen.NM_007364,4277
gen.NM_006833,2338	gen.NM_007372,4931
gen.NM_006835,1449	gen.NM_012068,5525
gen.NM_006837,2565	gen.NM_012098,2782
gen.NM_006839,814	gen.NM_012099,5504
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gen.NM_012101,3420 gen.NM_012111,4055 gen.NM_012112,5715 gen.NM_012116,5519 gen.NM_012138,4838 gen.NM_012170,4265 gen.NM_012170,4265 gen.NM_012170,6017 gen.NM_012181,5350 gen.NM_012203,2693 gen.NM_012207,2955 gen.NM_012237,5409 gen.NM_012248,4451 gen.NM_012248,4451 gen.NM_012255,5698 gen.NM_012264,6054 gen.NM_012286,6246 gen.NM_012296,3344 gen.NM_012296,3344 gen.NM_012323,6052 gen.NM_012323,6052 gen.NM_012412,2236 gen.NM_012412,2236 gen.NM_012443,5550 gen.NM_012443,5550 gen.NM_012458,5155 gen.NM_012469,5873 gen.NM_012469,5873 gen.NM_013237,1834 gen.NM_013247,801 gen.NM_013277,3566 gen.NM_013277,3566 gen.NM_013277,3566 gen.NM_013277,3566 gen.NM_013333,5617 gen.NM_013336,1238 gen.NM_013365,6032 gen.NM_013365,6032 gen.NM_013365,6032 gen.NM_013407,5270 gen.NM_013407,5270 gen.NM_013407,5270 gen.NM_013407,5270 gen.NM_013407,5270 gen.NM_013403,5492 gen.NM_014003,4592 gen.NM_014003,4592 gen.NM_014003,2551 gen.NM_014063,2251 gen.NM_014166,3906 gen.NM_014172,2862	,
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gen.XM_118637,4251	gen.XM_165717,1934 gen.XM_165728,2036
gen.XM_165390,3427	gen.XM_165738, 1999
gen.XM_165410,4583	gen.XM_165740, 1865
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gen.XM_165442,59	gen.XM_165771,1983
gen.XM_165443,477	gen.XM_165772,1876
gen.XM_165448,723	gen.XM_165777,2044
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gen.XM_165876,2258	gen.XM_166277,4532
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gen.XM_165882,2248	gen.XM_166285,4490
gen.XM_165888,2934	gen.XM_166288,5071
gen.XM_165890,2929	gen.XM_166303,2092
gen.XM_165891,2941	gen.XM_166310,2101
gen.XM_165903,3633	gen.XM_166327,2157
gen.XM_165905,3579	gen.XM_166333,1932
gen.XM_165906,3532	gen.XM_166336,2021
gen.XM_165910,3465	gen.XM_166340,1882
gen.XM_165921,4127	gen.XM_166349,1872
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gen.XM_165994,927	gen.XM_166406,2015
gen.XM_165998,893	gen.XM_166412,1910
gen.XM_166007,910	gen.XM_166417,1914
gen.XM_166008,900	gen.XM_166419,1920
gen.XM_166011,1121	gen.XM_166425,1888
gen.XM_166014,1275	gen.XM_166446,2042
gen.XM_166015,1192	gen.XM_166457,1878
gen.XM_166017,1350	gen.XM_166459, 1931
gen.XM_166026, 1669	gen.XM_166469, 1879
gen.XM_166027,1663	gen.XM_166480, 1955
gen.XM_166028,1842	gen.XM_166482,2351
gen.XM_166029,1802	gen.XM_166485,2353
gen.XM_166037,1612	gen.XM_166494,2224
gen.XM_166042,2054	gen.XM_166504,2222
gen.XM_166049,2147	gen.XM_166505,2202
gen.XM_166063,2540	gen.XM_166506,2200
gen.XM_166064,2558	gen.XM_166509,2219
gen.XM_166078,6142	gen.XM_166512,2205
gen.XM_166081,6255	gen.XM_166513,2220
gen.XM_166093,2984	gen.XM_166514,2203
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gen.XM_1670	27 2094
gen.XM_1670	37 2096
gen.XM_1670	M6 2150
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gen.XM_1672	225,2047
gen.XM_1673	39,2264
gen.XM_1673	
gen.XM_1673	•
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gen.XM_1673	111 2001
gen.XM_1674	11,2901
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gen.XM_1674	•
gen.XM_1674	39,3876
gen.XM_1674	53,4538
gen.XM_1674	56,4541
gen.XM_1674	
gen.XM_1674	77.2325
gen.XM_1674	
gen.XM_1674	
gen.XM_1674	•
gen VM 1674	09 2201
gen.XM_1674	90,2301
gen.XM_1675	00,2299
gen.XM_1675	02,2312
gen.XM_1675	04,2300
gen.XM_1675	18,3754
gen.XM_1675	
gen.XM_1675	38,5945
gen.XM_1675	58,2645
gen.XM_1676	
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gen.XM_1677	26 3248
gen.XM_1677	47 2721
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gen.XM_1678	
gen.XM_1678	53,3318
gen.XM_1678	92,3883
gen.XM_1679	

gen.XM_167911,3868 gen.XM_167918,3869 gen.XM_168054,2103 gen.XM_168070,1928 gen.XM_168104,1994 gen.XM_168123,1877 gen.XM_168181,2322 gen.XM_168251,2323 gen.XM_168354,2271 gen.XM_168378,2269 gen.XM_168435,2316 gen.XM_168450,2315 gen.XM_168454,2302 gen.XM_168461,2311 gen.XM_168464,2317 gen.XM_168470,2310 gen.XM_168548,2375 gen.XM_168572,2380 gen.XM_168586,2360 gen.XM_169414,3880 gen.XM_169540,5078 gen.XM_170195,2267 gen.XM_170427,2318

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. <u>Definitions</u>

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The terms "TAT polypeptide" and "TAT" as used herein and when immediately followed by a numerical designation, refer to various polypeptides, wherein the complete designation (i.e., TAT/number) refers to specific polypeptide sequences as described herein. The terms "TAT/number polypeptide" and "TAT/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides, polypeptide variants and fragments of native sequence polypeptides and polypeptide variants (which are further defined herein). The TAT polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "TAT polypeptide" refers to each individual TAT/number polypeptide disclosed herein. All disclosures in this specification which refer to the "TAT polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, formation of TAT binding oligopeptides to or against, formation of TAT binding organic molecules to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "TAT polypeptide" also includes variants of the TAT/number polypeptides disclosed herein.

A "native sequence TAT polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding TAT polypeptide derived from nature. Such native sequence TAT polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence TAT polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific TAT polypeptide (e.g., an extracellular domain sequence), naturally-occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In certain embodiments of the invention, the native sequence TAT polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons (if indicated) are shown in bold font and underlined in the figures. Nucleic acid residues indicated as "N" in the accompanying figures are any nucleic acid residue. However, while the TAT polypeptides disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the TAT polypeptides.

The TAT polypeptide "extracellular domain" or "ECD" refers to a form of the TAT polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a TAT polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the TAT polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an

extracellular domain of a TAT polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

The approximate location of the "signal peptides" of the various TAT polypeptides disclosed herein may be shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

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"TAT polypeptide variant" means a TAT polypeptide, preferably an active TAT polypeptide, as defined herein having at least about 80% amino acid sequence identity with a full-length native sequence TAT polypeptide sequence as disclosed herein, a TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length TAT polypeptide sequence as disclosed herein (such as those encoded by a nucleic acid that represents only a portion of the complete coding sequence for a full-length TAT polypeptide). Such TAT polypeptide variants include, for instance, TAT polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a TAT polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid sequence identity, to a full-length native sequence TAT polypeptide sequence as disclosed herein, a TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide sequence as disclosed herein. Ordinarily, TAT variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600 amino acids in length, or more. Optionally, TAT variant polypeptides will have no more than one conservative amino acid substitution as compared to the native TAT polypeptide sequence, alternatively no more than 2, 3, 4, 5, 6, 7, 8, 9, or 10 conservative amino acid substitution as compared to the native TAT polypeptide sequence.

"Percent (%) amino acid sequence identity" with respect to the TAT polypeptide sequences identified

herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific TAT polypeptide sequence, after aligning the sequences and introducing gaps. if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "TAT", wherein "TAT" represents the amino acid sequence of a hypothetical TAT polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "TAT" polypeptide of interest is being compared, and "X, "Y" and "Z" each represent different hypothetical amino acid residues. Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

"TAT variant polynucleotide" or "TAT variant nucleic acid sequence" means a nucleic acid molecule

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which encodes a TAT polypeptide, preferably an active TAT polypeptide, as defined herein and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence TAT polypeptide sequence as disclosed herein, a full-length native sequence TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length TAT polypeptide sequence as disclosed herein (such as those encoded by a nucleic acid that represents only a portion of the complete coding sequence for a full-length TAT polypeptide). Ordinarily, a TAT variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence TAT polypeptide sequence as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide as disclosed herein or any other fragment of a full-length TAT polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, TAT variant polynucleotides are at least about 5 nucleotides in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length.

"Percent (%) nucleic acid sequence identity" with respect to TAT-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the TAT nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison

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parameters are set by the ALIGN-2 program and do not vary.

may be those that are encoded by a TAT variant polynucleotide.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

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100 times the fraction W/Z

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be

the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "TAT-DNA", wherein "TAT-DNA" represents a hypothetical TAT-encoding nucleic

acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "TAT-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides. Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2

polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions. to nucleotide sequences encoding a full-length TAT polypeptide as disclosed herein. TAT variant polypeptides

polypeptide refers to the sequence of nucleotides which encode the full-length TAT polypeptide of the invention (which is often shown between start and stop codons, inclusive thereof, in the accompanying figures). The term "full-length coding region" when used in reference to an ATCC deposited nucleic acid refers to the TAT polypeptide-encoding portion of the cDNA that is inserted into the vector deposited with the ATCC (which is

In other embodiments, TAT variant polynucleotides are nucleic acid molecules that encode a TAT

The term "full-length coding region" when used in reference to a nucleic acid encoding a TAT

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appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate

computer program.

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often shown between start and stop codons, inclusive thereof, in the accompanying figures).

"Isolated," when used to describe the various TAT polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or.

preferably, silver stain. Isolated polypeptide includes polypeptide in situ within recombinant cells, since at least one component of the TAT polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" TAT polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium

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chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) overnight hybridization in a solution that employs 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with a 10 minute wash at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) followed by a 10 minute high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., <u>Molecular Cloning: A Laboratory Manual</u>, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent that those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a TAT polypeptide or anti-TAT antibody fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

"Active" or "activity" for the purposes herein refers to form(s) of a TAT polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring TAT, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring TAT other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring TAT and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring TAT.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native TAT polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native TAT polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native TAT polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a TAT polypeptide may comprise contacting a TAT polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities

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normally associated with the TAT polypeptide.

"Treating" or "treatment" or "alleviation" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented. A subject or mammal is successfully "treated" for a TAT polypeptide-expressing cancer if, after receiving a therapeutic amount of an anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule according to the methods of the present invention, the patient shows observable and/or measurable reduction in or absence of one or more of the following: reduction in the number of cancer cells or absence of the cancer cells; reduction in the tumor size; inhibition (i.e., slow to some extent and preferably stop) of cancer cell infiltration into peripheral organs including the spread of cancer into soft tissue and bone; inhibition (i.e., slow to some extent and preferably stop) of tumor metastasis; inhibition, to some extent, of tumor growth; and/or relief to some extent, one or more of the symptoms associated with the specific cancer; reduced morbidity and mortality, and improvement in quality of life issues. To the extent the anti-TAT antibody or TAT binding oligopeptide may prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic. Reduction of these signs or symptoms may also be felt by the patient.

The above parameters for assessing successful treatment and improvement in the disease are readily measurable by routine procedures familiar to a physician. For cancer therapy, efficacy can be measured, for example, by assessing the time to disease progression (TTP) and/or determining the response rate (RR). Metastasis can be determined by staging tests and by bone scan and tests for calcium level and other enzymes to determine spread to the bone. CT scans can also be done to look for spread to the pelvis and lymph nodes in the area. Chest X-rays and measurement of liver enzyme levels by known methods are used to look for metastasis to the lungs and liver, respectively. Other routine methods for monitoring the disease include transrectal ultrasonography (TRUS) and transrectal needle biopsy (TRNB).

For bladder cancer, which is a more localized cancer, methods to determine progress of disease include urinary cytologic evaluation by cystoscopy, monitoring for presence of blood in the urine, visualization of the urothelial tract by sonography or an intravenous pyelogram, computed tomography (CT) and magnetic resonance imaging (MRI). The presence of distant metastases can be assessed by CT of the abdomen, chest x-rays, or radionuclide imaging of the skeleton.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of the treatment of, alleviating the symptoms of or diagnosis of a cancer refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous

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(concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN®, polyethylene glycol (PEG), and PLURONICS®.

By "solid phase" or "solid support" is meant a non-aqueous matrix to which an antibody, TAT binding oligopeptide or TAT binding organic molecule of the present invention can adhere or attach. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a TAT polypeptide, an antibody thereto or a TAT binding oligopeptide) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

A "small" molecule or "small" organic molecule is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide, antibody, TAT binding oligopeptide, TAT binding organic molecule or an agonist or antagonist thereof as disclosed herein is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and in a routine manner, in relation to the stated purpose.

The term "therapeutically effective amount" refers to an amount of an antibody, polypeptide, TAT binding oligopeptide, TAT binding organic molecule or other drug effective to "treat" a disease or disorder in a subject or mammal. In the case of cancer, the therapeutically effective amount of the drug may reduce the number of cancer cells; reduce the tumor size; inhibit (i.e., slow to some extent and preferably stop) cancer cell infiltration into peripheral organs; inhibit (i.e., slow to some extent and preferably stop) tumor metastasis; inhibit, to some extent, tumor growth; and/or relieve to some extent one or more of the symptoms associated with the cancer. See the definition herein of "treating". To the extent the drug may prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic.

A "growth inhibitory amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide

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or TAT binding organic molecule is an amount capable of inhibiting the growth of a cell, especially tumor, e.g., cancer cell, either *in vitro* or *in vivo*. A "growth inhibitory amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide or TAT binding organic molecule for purposes of inhibiting neoplastic cell growth may be determined empirically and in a routine manner.

A "cytotoxic amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide or TAT binding organic molecule is an amount capable of causing the destruction of a cell, especially tumor, e.g., cancer cell, either *in vitro* or *in vivo*. A "cytotoxic amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide or TAT binding organic molecule for purposes of inhibiting neoplastic cell growth may be determined empirically and in a routine manner.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-TAT monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-TAT antibody compositions with polyepitopic specificity, polyclonal antibodies, single chain anti-TAT antibodies, and fragments of anti-TAT antibodies (see below) as long as they exhibit the desired biological or immunological activity. The term "immunoglobulin" (Ig) is used interchangeable with antibody herein.

An "isolated antibody" is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

The basic 4-chain antibody unit is a heterotetrameric glycoprotein composed of two identical light (L) chains and two identical heavy (H) chains (an IgM antibody consists of 5 of the basic heterotetramer unit along with an additional polypeptide called J chain, and therefore contain 10 antigen binding sites, while secreted IgA antibodies can polymerize to form polyvalent assemblages comprising 2-5 of the basic 4-chain units along with J chain). In the case of IgGs, the 4-chain unit is generally about 150,000 daltons. Each L chain is linked to a H chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype. Each H and L chain also has regularly spaced intrachain disulfide bridges. Each H chain has at the N-terminus, a variable domain (V_H) followed by three constant domains (V_H) for each of the α and γ chains and four V_H domains for μ and ε isotypes. Each L chain has at the N-terminus, a variable domain (V_L) followed by a constant domain (V_L) at its other end. The V_L is aligned with the V_H and the V_H and the V_L is aligned with the first constant domain of the heavy chain (V_L). Particular amino acid residues are believed to form an interface between the light chain and heavy chain variable domains. The pairing of a V_H and V_L together forms a single antigen-binding site. For the structure and properties of the

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different classes of antibodies, see, e.g., <u>Basic and Clinical Immunology</u>, 8th edition, Daniel P. Stites, Abba I. Terr and Tristram G. Parslow (eds.), Appleton & Lange, Norwalk, CT, 1994, page 71 and Chapter 6.

The L chain from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains. Depending on the amino acid sequence of the constant domain of their heavy chains (C_H) , immunoglobulins can be assigned to different classes or isotypes. There are five classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, having heavy chains designated α , δ , ϵ , γ , and μ , respectively. The γ and α classes are further divided into subclasses on the basis of relatively minor differences in C_H sequence and function, e.g., humans express the following subclasses: IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2.

The term "variable" refers to the fact that certain segments of the variable domains differ extensively in sequence among antibodies. The V domain mediates antigen binding and define specificity of a particular antibody for its particular antigen. However, the variability is not evenly distributed across the 110-amino acid span of the variable domains. Instead, the V regions consist of relatively invariant stretches called framework regions (FRs) of 15-30 amino acids separated by shorter regions of extreme variability called "hypervariable regions" that are each 9-12 amino acids long. The variable domains of native heavy and light chains each comprise four FRs, largely adopting a β-sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β-sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody dependent cellular cytotoxicity (ADCC).

The term "hypervariable region" when used herein refers to the amino acid residues of an antibody which are responsible for antigen-binding. The hypervariable region generally comprises amino acid residues from a "complementarity determining region" or "CDR" (e.g. around about residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the V_L, and around about 1-35 (H1), 50-65 (H2) and 95-102 (H3) in the V_H; Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)) and/or those residues from a "hypervariable loop" (e.g. residues 26-32 (L1), 50-52 (L2) and 91-96 (L3) in the V_L, and 26-32 (H1), 53-55 (H2) and 96-101 (H3) in the V_H; Chothia and Lesk J. Mol. Biol. 196:901-917 (1987)).

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to polyclonal antibody preparations which include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. In addition to their specificity, the monoclonal antibodies are advantageous in that they may be synthesized uncontaminated by other antibodies.

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The modifier "monoclonal" is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies useful in the present invention may be prepared by the hybridoma methodology first described by Kohler et al., Nature, 256:495 (1975), or may be made using recombinant DNA methods in bacterial, eukaryotic animal or plant cells (see, e.g., U.S. Patent No. 4,816,567). The "monoclonal antibodies" may also be isolated from phage antibody libraries using the techniques described in Clackson et al., Nature, 352:624-628 (1991) and Marks et al., J. Mol. Biol., 222:581-597 (1991), for example.

The monoclonal antibodies herein include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (see U.S. Patent No. 4,816,567; and Morrison et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984)). Chimeric antibodies of interest herein include "primatized" antibodies comprising variable domain antigen-binding sequences derived from a non-human primate (e.g. Old World Monkey, Ape etc), and human constant region sequences.

An "intact" antibody is one which comprises an antigen-binding site as well as a C_L and at least heavy chain constant domains, C_H1 , C_H2 and C_H3 . The constant domains may be native sequence constant domains (e.g. human native sequence constant domains) or amino acid sequence variant thereof. Preferably, the intact antibody has one or more effector functions.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab') 2, and Fv fragments; diabodies; linear antibodies (see U.S. Patent No. 5,641,870, Example 2; Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. The Fab fragment consists of an entire L chain along with the variable region domain of the H chain (V_H) , and the first constant domain of one heavy chain (C_H1) . Each Fab fragment is monovalent with respect to antigen binding, i.e., it has a single antigen-binding site. Pepsin treatment of an antibody yields a single large F(ab') fragment which roughly corresponds to two disulfide linked Fab fragments having divalent antigen-binding activity and is still capable of cross-linking antigen. Fab' fragments differ from Fab fragments by having additional few residues at the carboxy terminus of the C_H1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab') antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The Fc fragment comprises the carboxy-terminal portions of both H chains held together by disulfides.

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The effector functions of antibodies are determined by sequences in the Fc region, which region is also the part recognized by Fc receptors (FcR) found on certain types of cells.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This fragment consists of a dimer of one heavy- and one light-chain variable region domain in tight, non-covalent association. From the folding of these two domains emanate six hypervariable loops (3 loops each from the H and L chain) that contribute the amino acid residues for antigen binding and confer antigen binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

"Single-chain Fv" also abbreviated as "sFv" or "scFv" are antibody fragments that comprise the V_H and V_L antibody domains connected into a_l single polypeptide chain. Preferably, the sFv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994); Borrebaeck 1995, infra.

The term "diabodies" refers to small antibody fragments prepared by constructing sFv fragments (see preceding paragraph) with short linkers (about 5-10 residues) between the V_H and V_L domains such that interchain but not intra-chain pairing of the V domains is achieved, resulting in a bivalent fragment, i.e., fragment having two antigen-binding sites. Bispecific diabodies are heterodimers of two "crossover" sFv fragments in which the V_H and V_L domains of the two antibodies are present on different polypeptide chains. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

"Humanized" forms of non-human (e.g., rodent) antibodies are chimeric antibodies that contain minimal sequence derived from the non-human antibody. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region of the recipient are replaced by residues from a hypervariable region of a non-human species (donor antibody) such as mouse, rat, rabbit or non-human primate having the desired antibody specificity, affinity, and capability. In some instances, framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the hypervariable loops correspond to those of a non-human immunoglobulin and all or substantially all of the FRs are those of a human immunoglobulin sequence. The humanized antibody optionally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones et al., Nature 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol. 2:593-596 (1992).

A "species-dependent antibody," e.g., a mammalian anti-human IgE antibody, is an antibody which

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has a stronger binding affinity for an antigen from a first mammalian species than it has for a homologue of that antigen from a second mammalian species. Normally, the species-dependent antibody "bind specifically" to a human antigen (i.e., has a binding affinity (Kd) value of no more than about 1 x 10⁻⁷ M, preferably no more than about 1 x 10⁻⁸ and most preferably no more than about 1 x 10⁻⁹ M) but has a binding affinity for a homologue of the antigen from a second non-human mammalian species which is at least about 50 fold, or at least about 500 fold, or at least about 1000 fold, weaker than its binding affinity for the human antigen. The species-dependent antibody can be of any of the various types of antibodies as defined above, but preferably is a humanized or human antibody.

A "TAT binding oligopeptide" is an oligopeptide that binds, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be chemically synthesized using known oligopeptide synthesis methodology or may be prepared and purified using recombinant technology. TAT binding oligopeptides are usually at least about 5 amino acids in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length or more, wherein such oligopeptides that are capable of binding, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening oligopeptide libraries for oligopeptides that are capable of specifically binding to a polypeptide target are well known in the art (see, e.g., U.S. Patent Nos. 5,556,762, 5,750,373, 4,708,871, 4,833,092, 5,223,409, 5,403,484, 5,571,689, 5,663,143; PCT Publication Nos. WO 84/03506 and WO84/03564; Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 81:3998-4002 (1984); Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 82:178-182 (1985); Geysen et al., in Synthetic Peptides as Antigens, 130-149 (1986); Geysen et al., J. Immunol. Meth., 102:259-274 (1987); Schoofs et al., J. Immunol., 140:611-616 (1988), Cwirla, S. E. et al. (1990) Proc. Natl. Acad. Sci. USA, 87:6378; Lowman, H.B. et al. (1991) Biochemistry, 30:10832; Clackson, T. et al. (1991) Nature, 352: 624; Marks, J. D. et al. (1991), J. Mol. Biol., 222:581; Kang, A.S. et al. (1991) Proc. Natl. Acad. Sci. USA, 88:8363, and Smith, G. P. (1991) Current Opin. Biotechnol., 2:668).

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A "TAT binding organic molecule" is an organic molecule other than an oligopeptide or antibody as defined herein that binds, preferably specifically, to a TAT polypeptide as described herein. TAT binding organic molecules may be identified and chemically synthesized using known methodology (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585). TAT binding organic molecules are usually less than about 2000 daltons in size, alternatively less than about 1500, 750, 500, 250 or 200 daltons in size, wherein such organic molecules that are capable of binding, preferably specifically, to a TAT polypeptide as described herein may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening organic molecule libraries for molecules that are capable of binding to a polypeptide target are well known in the art (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585).

An antibody, oligopeptide or other organic molecule "which binds" an antigen of interest, e.g. a tumorassociated polypeptide antigen target, is one that binds the antigen with sufficient affinity such that the antibody, oligopeptide or other organic molecule is useful as a diagnostic and/or therapeutic agent in targeting a cell or tissue expressing the antigen, and does not significantly cross-react with other proteins. In such embodiments, the extent of binding of the antibody, oligopeptide or other organic molecule to a "non-target" protein will be less than about 10% of the binding of the antibody, oligopeptide or other organic molecule to its particular target protein as determined by fluorescence activated cell sorting (FACS) analysis or radioimmunoprecipitation (RIA). With regard to the binding of an antibody, oligopeptide or other organic molecule to a target molecule, the term "specific binding" or "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide target means binding that is measurably different from a non-specific interaction. Specific binding can be measured, for example, by determining binding of a molecule compared to binding of a control molecule, which generally is a molecule of similar structure that does not have binding activity. For example, specific binding can be determined by competition with a control molecule that is similar to the target, for example, an excess of non-labeled target. In this case, specific binding is indicated if the binding of the labeled target to a probe is competitively inhibited by excess unlabeled target. The term "specific binding" or "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide target as used herein can be exhibited, for example, by a molecule having a Kd for the target of at least about 10⁻⁴ M, alternatively at least about 10⁻⁵ M, alternatively at least about 10⁻⁶ M, alternatively at least about 10⁻⁷ M, alternatively at least about 10⁻⁸ M, alternatively at least about 10⁻⁹ M, alternatively at least about 10⁻¹⁰ M, alternatively at least about 10⁻¹¹ M, alternatively at least about 10⁻¹² M, or greater. In one embodiment, the term "specific binding" refers to binding where a molecule binds to a particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

An antibody, oligopeptide or other organic molecule that "inhibits the growth of tumor cells expressing a TAT polypeptide" or a "growth inhibitory" antibody, oligopeptide or other organic molecule is one which results in measurable growth inhibition of cancer cells expressing or overexpressing the appropriate TAT polypeptide. The TAT polypeptide may be a transmembrane polypeptide expressed on the surface of a cancer cell or may be a polypeptide that is produced and secreted by a cancer cell. Preferred growth inhibitory anti-TAT antibodies, oligopeptides or organic molecules inhibit growth of TAT-expressing tumor cells by greater

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than 20%, preferably from about 20% to about 50%, and even more preferably, by greater than 50% (e.g., from about 50% to about 100%) as compared to the appropriate control, the control typically being tumor cells not treated with the antibody, oligopeptide or other organic molecule being tested. In one embodiment, growth inhibition can be measured at an antibody concentration of about 0.1 to 30 μ g/ml or about 0.5 nM to 200 nM in cell culture, where the growth inhibition is determined 1-10 days after exposure of the tumor cells to the antibody. Growth inhibition of tumor cells *in vivo* can be determined in various ways such as is described in the Experimental Examples section below. The antibody is growth inhibitory in vivo if administration of the anti-TAT antibody at about 1 μ g/kg to about 100 mg/kg body weight results in reduction in tumor size or tumor cell proliferation within about 5 days to 3 months from the first administration of the antibody, preferably within about 5 to 30 days.

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An antibody, oligopeptide or other organic molecule which "induces apoptosis" is one which induces programmed cell death as determined by binding of annexin V, fragmentation of DNA, cell shrinkage, dilation of endoplasmic reticulum, cell fragmentation, and/or formation of membrane vesicles (called apoptotic bodies). The cell is usually one which overexpresses a TAT polypeptide. Preferably the cell is a tumor cell, e.g., a prostate, breast, ovarian, stomach, endometrial, lung, kidney, colon, bladder cell. Various methods are available for evaluating the cellular events associated with apoptosis. For example, phosphatidyl serine (PS) translocation can be measured by annexin binding; DNA fragmentation can be evaluated through DNA laddering; and nuclear/chromatin condensation along with DNA fragmentation can be evaluated by any increase in hypodiploid cells. Preferably, the antibody, oligopeptide or other organic molecule which induces apoptosis is one which results in about 2 to 50 fold, preferably about 5 to 50 fold, and most preferably about 10 to 50 fold, induction of annexin binding relative to untreated cell in an annexin binding assay.

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Antibody "effector functions" refer to those biological activities attributable to the Fc region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody, and vary with the antibody isotype. Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (e.g., B cell receptor); and B cell activation.

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"Antibody-dependent cell-mediated cytotoxicity" or "ADCC" refers to a form of cytotoxicity in which secreted Ig bound onto Fc receptors (FcRs) present on certain cytotoxic cells (e.g., Natural Killer (NK) cells, neutrophils, and macrophages) enable these cytotoxic effector cells to bind specifically to an antigen-bearing target cell and subsequently kill the target cell with cytotoxins. The antibodies "arm" the cytotoxic cells and are absolutely required for such killing. The primary cells for mediating ADCC, NK cells, express Fc \(\gamma \)RIII only, whereas monocytes express Fc\(\gamma \)RII and Fc\(\gamma \)RIII. FcR expression on hematopoietic cells is summarized in Table 3 on page 464 of Ravetch and Kinet, \(\frac{Annu. Rev. Immunol.}{Annu. Rev. 19:457-92} \) (1991). To assess ADCC activity of a molecule of interest, an in vitro ADCC assay, such as that described in US Patent No. 5,500,362 or 5,821,337 may be performed. Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed in vivo, e.g., in a animal model such as that disclosed in Clynes et al.

(USA) 95:652-656 (1998).

"Fc receptor" or "FcR" describes a receptor that binds to the Fc region of an antibody. The preferred FcR is a native sequence human FcR. Moreover, a preferred FcR is one which binds an IgG antibody (a gamma receptor) and includes receptors of the FcγRI, FcγRII and FcγRIII subclasses, including allelic variants and alternatively spliced forms of these receptors. FcγRII receptors include FcγRIIA (an "activating receptor") and FcγRIIB (an "inhibiting receptor"), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Activating receptor Fc γRIIA contains an immunoreceptor tyrosine-based activation motif (ITAM) in its cytoplasmic domain. Inhibiting receptor FcγRIIB contains an immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain. (see review M. in Daëron, Annu. Rev. Immunol. 15:203-234 (1997)). FcRs are reviewed in Ravetch and Kinet, Annu. Rev. Immunol. 9:457-492 (1991); Capel et al., Immunomethods 4:25-34 (1994); and de Haas et al., J. Lab. Clin. Med. 126:330-41 (1995). Other FcRs, including those to be identified in the future, are encompassed by the term "FcR" herein. The term also includes the neonatal receptor, FcRn, which is responsible for the transfer of maternal IgGs to the fetus (Guyer et al., J. Immunol. 117:587 (1976) and Kim et al., J. Immunol. 24:249 (1994)).

"Human effector cells" are leukocytes which express one or more FcRs and perform effector functions. Preferably, the cells express at least Fc γRIII and perform ADCC effector function. Examples of human leukocytes which mediate ADCC include peripheral blood mononuclear cells (PBMC), natural killer (NK) cells, monocytes, cytotoxic T cells and neutrophils; with PBMCs and NK cells being preferred. The effector cells may be isolated from a native source, e.g., from blood.

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"Complement dependent cytotoxicity" or "CDC" refers to the lysis of a target cell in the presence of complement. Activation of the classical complement pathway is initiated by the binding of the first component of the complement system (C1q) to antibodies (of the appropriate subclass) which are bound to their cognate antigen. To assess complement activation, a CDC assay, e.g., as described in Gazzano-Santoro et al., <u>J. Immunol. Methods</u> 202:163 (1996), may be performed.

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The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include, but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia or lymphoid malignancies. More particular examples of such cancers include squamous cell cancer (e.g., epithelial squamous cell cancer), lung cancer including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung and squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, cancer of the urinary tract, hepatoma, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, melanoma, multiple myeloma and B-cell lymphoma, brain, as well as head and neck cancer, and associated metastases.

The terms "cell proliferative disorder" and "proliferative disorder" refer to disorders that are

associated with some degree of abnormal cell proliferation. In one embodiment, the cell proliferative disorder is cancer.

"Tumor", as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues.

An antibody, oligopeptide or other organic molecule which "induces cell death" is one which causes a viable cell to become nonviable. The cell is one which expresses a TAT polypeptide, preferably a cell that overexpresses a TAT polypeptide as compared to a normal cell of the same tissue type. The TAT polypeptide may be a transmembrane polypeptide expressed on the surface of a cancer cell or may be a polypeptide that is produced and secreted by a cancer cell. Preferably, the cell is a cancer cell, e.g., a breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, thyroid, pancreatic or bladder cell. Cell death *in vitro* may be determined in the absence of complement and immune effector cells to distinguish cell death induced by antibody-dependent cell-mediated cytotoxicity (ADCC) or complement dependent cytotoxicity (CDC). Thus, the assay for cell death may be performed using heat inactivated serum (i.e., in the absence of complement) and in the absence of immune effector cells. To determine whether the antibody, oligopeptide or other organic molecule is able to induce cell death, loss of membrane integrity as evaluated by uptake of propidium iodide (PI), trypan blue (see Moore et al. Cytotechnology 17:1-11 (1995)) or 7AAD can be assessed relative to untreated cells. Preferred cell death-inducing antibodies, oligopeptides or other organic molecules are those which induce PI uptake in the PI uptake assay in BT474 cells.

A "TAT-expressing cell" is a cell which expresses an endogenous or transfected TAT polypeptide either on the cell surface or in a secreted form. A "TAT-expressing cancer" is a cancer comprising cells that have a TAT polypeptide present on the cell surface or that produce and secrete a TAT polypeptide. A "TATexpressing cancer" optionally produces sufficient levels of TAT polypeptide on the surface of cells thereof, such that an anti-TAT antibody, oligopeptide of other organic molecule can bind thereto and have a therapeutic effect with respect to the cancer. In another embodiment, a "TAT-expressing cancer" optionally produces and secretes sufficient levels of TAT polypeptide, such that an anti-TAT antibody, oligopeptide ot other organic molecule antagonist can bind thereto and have a therapeutic effect with respect to the cancer. With regard to the latter, the antagonist may be an antisense oligonucleotide which reduces, inhibits or prevents production and secretion of the secreted TAT polypeptide by tumor cells. A cancer which "overexpresses" a TAT polypeptide is one which has significantly higher levels of TAT polypeptide at the cell surface thereof, or produces and secretes, compared to a noncancerous cell of the same tissue type. Such overexpression may be caused by gene amplification or by increased transcription or translation. TAT polypeptide overexpression may be determined in a diagnostic or prognostic assay by evaluating increased levels of the TAT protein present on the surface of a cell, or secreted by the cell (e.g., via an immunohistochemistry assay using anti-TAT antibodies prepared against an isolated TAT polypeptide which may be prepared using recombinant DNA technology from an isolated nucleic acid encoding the TAT polypeptide; FACS analysis, etc.). Alternatively, or additionally, one may measure levels of TAT polypeptide-encoding nucleic acid or mRNA in the cell, e.g., via fluorescent in situ hybridization using a nucleic acid based probe corresponding to a TAT-encoding nucleic acid or the complement

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thereof; (FISH; see WO98/45479 published October, 1998), Southern blotting, Northern blotting, or polymerase chain reaction (PCR) techniques, such as real time quantitative PCR (RT-PCR). One may also study TAT polypeptide overexpression by measuring shed antigen in a biological fluid such as serum, e.g., using antibody-based assays (see also, e.g., U.S. Patent No. 4,933,294 issued June 12, 1990; WO91/05264 published April 18, 1991; U.S. Patent 5,401,638 issued March 28, 1995; and Sias et al., J. Immunol. Methods 132:73-80 (1990)). Aside from the above assays, various *in vivo* assays are available to the skilled practitioner. For example, one may expose cells within the body of the patient to an antibody which is optionally labeled with a detectable label, e.g., a radioactive isotope, and binding of the antibody to cells in the patient can be evaluated, e.g., by external scanning for radioactivity or by analyzing a biopsy taken from a patient previously exposed to the antibody.

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As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

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The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody, oligopeptide or other organic molecule so as to generate a "labeled" antibody, oligopeptide or other organic molecule. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

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The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes (e.g., Al, I¹³¹, I¹²⁵, Y⁹⁰, Re¹⁸⁶, Re¹⁸⁸, Sm¹⁵³, Bi²¹², P³² and radioactive isotopes of Lu), chemotherapeutic agents e.g. methotrexate, adriamicin, vinca alkaloids (vincristine, vinblastine, etoposide), doxorubicin, melphalan, mitomycin C, chlorambucil, daunorubicin or other intercalating agents, enzymes and fragments thereof such as nucleolytic enzymes, antibiotics, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof, and the various antitumor or anticancer agents disclosed below. Other cytotoxic agents are described below. A tumoricidal agent causes destruction of tumor cells.

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A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell, especially a TAT-expressing cancer cell, either *in vitro* or *in vivo*. Thus, the growth inhibitory agent may be one which significantly reduces the percentage of TAT-expressing cells in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such

as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxanes, and topoisomerase II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further information can be found in The Molecular Basis of Cancer, Mendelsohn and Israel, eds., Chapter 1, entitled "Cell cycle regulation, oncogenes, and antineoplastic drugs" by Murakami et al. (WB Saunders: Philadelphia, 1995), especially p. 13. The taxanes (paclitaxel and docetaxel) are anticancer drugs both derived from the yew tree. Docetaxel (TAXOTERE®, Rhone-Poulenc Rorer), derived from the European yew, is a semisynthetic analogue of paclitaxel (TAXOL®, Bristol-Myers Squibb). Paclitaxel and docetaxel promote the assembly of microtubules from tubulin dimers and stabilize microtubules by preventing depolymerization, which results in the inhibition of mitosis in cells.

"Doxorubicin" is an anthracycline antibiotic. The full chemical name of doxorubicin is (8S-cis)-10-[(3-amińo-2,3,6-trideoxy α -L-lyxo-hexapyranosyl)oxy]-7,8,9,10-tetrahydro-6,8,11-trihydroxy-8-(hydroxyacetyl)-1-methoxy-5,12-naphthacenedione.

The term "cytokine" is a generic term for proteins released by one cell population which act on another cell as intercellular mediators. Examples of such cytokines are lymphokines, monokines, and traditional polypeptide hormones. Included among the cytokines are growth hormone such as human growth hormone, Nmethionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroxine; insulin; proinsulin; relaxin; prorelaxin; glycoprotein hormones such as follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH), and luteinizing hormone (LH); hepatic growth factor; fibroblast growth factor; prolactin; placental lactogen; tumor necrosis factor- α and - β ; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors such as NGF-β; platelet-growth factor; transforming growth factors (TGFs) such as TGF- α and TGF- β ; insulin-like growth factor-I and -II; erythropoietin (EPO); osteoinductive factors; interferons such as interferon $-\alpha$, $-\beta$, and $-\gamma$; colony stimulating factors (CSFs) such as macrophage-CSF (M-CSF); granulocyte-macrophage-CSF (GM-CSF); and granulocyte-CSF (G-CSF); interleukins (ILs) such as IL-1, IL- 1a, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-11, IL-12; a tumor necrosis factor such as TNF- α or TNF-B; and other polypeptide factors including LIF and kit ligand (KL). As used herein, the term cytokine includes proteins from natural sources or from recombinant cell culture and biologically active equivalents of the native sequence cytokines.

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The term "package insert" is used to refer to instructions customarily included in commercial packages of therapeutic products, that contain information about the indications, usage, dosage, administration, contraindications and/or warnings concerning the use of such therapeutic products.

Table 1

```
/*
           * C-C increased from 12 to 15
           * Z is average of EQ
 5
           * B is average of ND
           * match with stop is M; stop-stop = 0; J (joker) match = 0
           */
          #define M
                                       /* value of a match with a stop */
10
          int
                     day[26][26] = {
                  ABCDEFGHIJKLMNOPQRSTUVWXYZ*/
          /* A */
                      \{2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0\},\
          /* B */
                      {0, 3,-4, 3, 2,-5, 0, 1,-2, 0, 0,-3,-2, 2, M,-1, 1, 0, 0, 0, 0, -2,-5, 0,-3, 1},
          /* C */
                      {-2,-4,15,-5,-5,-4,-3,-3,-2, 0,-5,-6,-5,-4,_M,-3,-5,-4, 0,-2, 0,-2,-8, 0, 0,-5},
                      {0, 3,-5, 4, 3,-6, 1, 1,-2, 0, 0,-4,-3, 2, M,-1, 2,-1, 0, 0, 0,-2,-7, 0,-4, 2}, {0, 2,-5, 3, 4,-5, 0, 1,-2, 0, 0,-3,-2, 1, M,-1, 2,-1, 0, 0, 0,-2,-7, 0,-4, 3},
15
          /* D */
          /* E */
          /* F */
                      {-4,-5,-4,-6,-5, 9,-5,-2, 1, 0,-5, 2, 0,-4, M,-5,-5,-4,-3,-3, 0,-1, 0, 0, 7,-5},
                      { 1, 0,-3, 1, 0,-5, 5,-2,-3, 0,-2,-4,-3, 0, M,-1,-1,-3, 1, 0, 0,-1,-7, 0,-5, 0},
          /* G */
          /* H */
                      {-1, 1,-3, 1, 1,-2,-2, 6,-2, 0, 0,-2,-2, 2, M, 0, 3, 2,-1,-1, 0,-2,-3, 0, 0, 2},
20
                      {-1,-2,-2,-2,-1,-3,-2, 5, 0,-2, 2, 2,-2, M,-2,-2,-1, 0, 0, 4,-5, 0,-1,-2},
           /* I */
                      /* J */
                      {-1, 0,-5, 0, 0,-5,-2, 0,-2, 0, 5,-3, 0, 1, M,-1, 1, 3, 0, 0, 0,-2,-3, 0,-4, 0},
           /* K */
                      {-2,-3,-6,-4,-3, 2,-4,-2, 2, 0,-3, 6, 4,-3,_M,-3,-2,-3,-1, 0, 2,-2, 0,-1,-2},
           /* L */
                      {-1,-2,-5,-3,-2, 0,-3,-2, 2, 0, 0, 4, 6,-2, M,-2,-1, 0,-2,-1, 0, 2,-4, 0,-2,-1}, { 0, 2,-4, 2, 1,-4, 0, 2,-2, 0, 1,-3,-2, 2, M,-1, 1, 0, 1, 0, 0,-2,-4, 0,-2, 1},
           /* M */
25
           /* N */
                      /* O */
           /* P */
                      \{1,-1,-3,-1,-1,-5,-1,0,-2,0,-1,-3,-2,-1,M,6,0,0,1,0,0,-1,-6,0,-5,0\},
           /* O */
                      \{0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3\},\
           /* R */
                      {-2, 0,-4,-1,-1,-4,-3, 2,-2, 0, 3,-3, 0, 0, M, 0, 1, 6, 0,-1, 0,-2, 2, 0,-4, 0},
                      { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
30
           /* S */
                      { 1, 0,-2, 0, 0,-3, 0,-1, 0, 0, 0,-1,-1, 0, M, 0,-1,-1, 1, 3, 0, 0,-5, 0,-3, 0},
           /* T */
           /* U */
                      { 0,-2,-2,-2,-1,-1,-2, 4, 0,-2, 2, 2,-2, M,-1,-2,-2,-1, 0, 0, 4,-6, 0,-2,-2}, {-6,-5,-8,-7,-7, 0,-7,-3,-5, 0,-3,-2,-4,-4, M,-6,-5, 2,-2,-5, 0,-6,17, 0, 0,-6},
           /* V */
           /* W */
                       /* X */
35
           /* Y */
                       {-3,-3, 0,-4,-4, 7,-5, 0,-1, 0,-4,-1,-2,-2, M,-5,-4,-4,-3,-3, 0,-2, 0, 0,10,-4},
           /* Z */
                       { 0, 1,-5, 2, 3,-5, 0, 2,-2, 0, 0,-2,-1, 1, M, 0, 3, 0, 0, 0, 0,-2,-6, 0,-4, 4}
           };
40
```

45

```
*/
           #include <stdio.h>
           #include <ctype.h>
  5
           #define MAXJMP
                                        16
                                                  /* max jumps in a diag */
           #define MAXGAP
                                        24
                                                  /* don't continue to penalize gaps larger than this */
           #define JMPS
                                        1024
                                                  /* max jmps in an path */
           #define MX
                                                  /* save if there's at least MX-1 bases since last jmp */
                                        4
10
           #define DMAT
                                        3
                                                  /* value of matching bases */
           #define DMIS
                                        0
                                                  /* penalty for mismatched bases */
           #define DINSO
                                        8
                                                  /* penalty for a gap */
           #define DINS1
                                                  /* penalty per base */
                                        1
15
           #define PINSO
                                        8
                                                  /* penalty for a gap */
           #define PINS1
                                        4
                                                  /* penalty per residue */
           struct jmp {
                                        n[MAXJMP]:
                                                            /* size of jmp (neg for dely) */
20
                    unsigned short
                                        x[MAXJMP];
                                                           /* base no. of jmp in seq x */
           };
                                                            /* limits seq to 2^16 -1 */
           struct diag {
                                        score;
                                                           /* score at last jmp */
25
                    long
                                        offset:
                                                           /* offset of prev block */
                    short
                                        ijmp;
                                                           /* current imp index */
                    struct jmp
                                        jp;
                                                           /* list of imps */
           };
30
           struct path {
                    int
                                                 /* number of leading spaces */
                              n[JMPS]; /* size of jmp (gap) */
                    short
                              x[JMPS]; /* loc of jmp (last elem before gap) */
           };
35
                              *ofile;
           char
                                                           /* output file name */
           char
                              *namex[2];
                                                           /* seq names: getseqs() */
           char
                              *prog;
                                                           /* prog name for err msgs */
           char
                              *seqx[2];
                                                           /* seqs: getseqs() */
40
           int
                                                           /* best diag: nw() */
                              dmax;
           int
                              dmax0;
                                                           /* final diag */
           int
                              dna;
                                                           /* set if dna: main() */
                                                           /* set if penalizing end gaps */
           int
                              endgaps;
           int
                              gapx, gapy;
                                                           /* total gaps in seqs */
45
           int
                              len0, len1;
                                                           /* seq lens */
           int
                                                           /* total size of gaps */
                              ngapx, ngapy;
           int
                              smax:
                                                           /* max score: nw() */
           int
                              *xbm;
                                                           /* bitmap for matching */
          long
                              offset;
                                                           /* current offset in jmp file */
50
          struct
                    diag
                              *dx;
                                                           /* holds diagonals */
          struct
                    path
                              pp[2];
                                                           /* holds path for seqs */
                              *calloc(), *malloc(), *index(), *strcpy();
          char
          char
                              *getseq(), *g_calloc();
```

```
/* Needleman-Wunsch alignment program
            * usage: progs file1 file2
               where file1 and file2 are two dna or two protein sequences.
  5
               The sequences can be in upper- or lower-case an may contain ambiguity
               Any lines beginning with ';', '>' or '<' are ignored

Max file length is 65535 (limited by unsigned short x in the jmp struct)
               A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
               Output is in the file "align.out"
10
            * The program may create a tmp file in /tmp to hold info about traceback.
            * Original version developed under BSD 4.3 on a vax 8650
           #include "nw.h"
15
           #include "day.h"
           static
                    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
           };
20
           static
                     pbval[26] = {
                    1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
                    128, 256, 0xFFFFFFF, 1 < < 10, 1 < < 11, 1 < < 12, 1 < < 13, 1 < < 14,
                    1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
25
                    1 < <23, 1 < <24, 1 < <25 | (1 < <('E'-'A')) | (1 < <('Q'-'A'))
           };
           main(ac, av)
                                                                                                                             main
                    int
                              ac;
30
                    char
                              *av[];
           {
                    prog = av[0];
                    if (ac != 3)  {
                              fprintf(stderr, "usage: %s file1 file2\n", prog);
35
                              fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
                              fprintf(stderr, "The sequences can be in upper- or lower-case\n");
                              fprintf(stderr, "Any lines beginning with ';' or '<' are ignored\n");
                              fprintf(stderr, "Output is in the file \"align.out\"\n");
                              exit(1);
40
                    namex[0] = av[1];
                    namex[1] = av[2];
                    seqx[0] = getseq(namex[0], \&len0);
                    seqx[1] = getseq(namex[1], &len1);
45
                    xbm = (dna)? dbval : pbval;
                    endgaps = 0;
                                                  /* 1 to penalize endgaps */
                    ofile = "align.out";
                                                           /* output file */
50
                                        /* fill in the matrix, get the possible jmps */
                    readjmps();
                                        /* get the actual imps */
                    print();
                                        /* print stats, alignment */
                    cleanup(0);
                                        /* unlink any tmp files */}
```

```
/* do the alignment, return best score: main()
           * dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
           * pro: PAM 250 values
           * When scores are equal, we prefer mismatches to any gap, prefer
 5
           * a new gap to extending an ongoing gap, and prefer a gap in seqx
           * to a gap in seq y.
           */
          nw()
                                                                                                                              nw
          {
10
                                                          /* seqs and ptrs */
                    char
                                       *px, *py;
                    int
                                       *ndely, *dely;
                                                          /* keep track of dely */
                                                          /* keep track of delx */
                    int
                                       ndelx, delx;
                                                          /* for swapping row0, row1 */
                    int
                                       *tmp;
                    int
                                       mis;
                                                          /* score for each type */
15
                                                          /* insertion penalties */
                    int
                                       ins0, ins1;
                                       id;
                                                          /* diagonal index */
                    register
                    register
                                                          /* jmp index */
                                       ij;
                    register
                                        *col0, *col1;
                                                          /* score for curr, last row */
                    register
                                                          /* index into seqs */
                                       xx, yy;
20
                    dx = (struct diag *)g calloc("to get diags", len0+len1+1, sizeof(struct diag));
                    ndely = (int *)g calloc("to get ndely", len1+1, sizeof(int));
                    dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
                    col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
25
                    col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
                    ins0 = (dna)? DINS0 : PINS0;
                    ins1 = (dna)? DINS1: PINS1;
                    smax = -10000;
                    if (endgaps) {
30
                              for (col0[0] = dely[0] = -ins0, yy = 1; yy < = len1; yy + +) {
                                       col0[yy] = dely[yy] = col0[yy-1] - ins1;
                                       ndely[yy] = yy;
                              col0[0] = 0;
                                                 /* Waterman Bull Math Biol 84 */
35
                    }
                    else
                              for (yy = 1; yy \le len1; yy++)
                                        dely[yy] = -ins0;
                    /* fill in match matrix
40
                    for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
                              /* initialize first entry in col
                              if (endgaps) {
45
                                        if (xx == 1)
                                                 col1[0] = delx = -(ins0+ins1);
                                        else
                                                 col1[0] = delx = col0[0] - ins1;
                                        ndelx = xx;
50
                              }
                              else {
                                        col1[0] = 0;
                                        delx = -ins0;
                                        ndelx = 0;
55
                              }
```

```
...nw
                            for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
                                      mis = col0[yy-1];
                                      if (dna)
 5
                                               mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
                                      else
                                               mis += day[*px-'A'][*py-'A'];
                                      /* update penalty for del in x seq;
10
                                      * favor new del over ongong del
                                      * ignore MAXGAP if weighting endgaps
                                      if (endgaps | | ndely[yy] < MAXGAP) {
                                               if (col0[yy] - ins0 > = dely[yy]) {
15
                                                        dely[yy] = col0[yy] - (ins0 + ins1);
                                                        ndely[yy] = 1;
                                               } else {
                                                        dely[yy] -= ins1;
                                                        ndely[yy]++;
20
                                               }
                                      } else {
                                               if (colO[yy] - (ins0 + ins1) > = dely[yy]) {
                                                        dely[yy] = col0[yy] - (ins0+ins1);
                                                        ndely[yy] = 1;
25
                                               } else
                                                        ndely[yy]++;
                                      }
                                      /* update penalty for del in y seq;
30
                                      * favor new del over ongong del
                                      if (endgaps | | ndelx < MAXGAP) {
                                               if (col1[yy-1] - ins0 > = delx) {
                                                        delx = col1[yy-1] - (ins0+ins1);
35
                                                        ndelx = 1;
                                               } else {
                                                        delx -= ins1;
                                                        ndelx++;
                                               }
40
                                      } else {
                                               if (col1[yy-1] - (ins0+ins1) > = delx) {
                                                        delx = col1[yy-1] - (ins0+ins1);
                                                        ndelx = 1;
                                               } else
45
                                                        ndelx++;
                                      }
                                      /* pick the maximum score; we're favoring
                                       * mis over any del and delx over dely
50
                                                                                                                      ...nw
                                      id = xx - yy + len1 - 1;
                                      if (mis > = delx && mis > = dely[yy])
55
                                               coll[yy] = mis;
```

```
Table 1 (cont')
                                      else if (delx > = dely[yy]) {
                                               coll[yy] = delx;
                                               ij = dx[id].ijmp;
                                               if (dx[id].jp.n[0] && (!dna | | (ndelx > = MAXJMP))
 5
                                               && xx > dx[id].jp.x[ij]+MX) \mid mis > dx[id].score+DINS0)) {
                                                        dx[id].ijmp++;
                                                        if (++ij > = MAXJMP) {
                                                                  writejmps(id);
                                                                  ij = dx[id].ijmp = 0;
10
                                                                  dx[id].offset = offset;
                                                                  offset += sizeof(struct jmp) + sizeof(offset);
                                                        }
                                               dx[id].jp.n[ij] = ndelx;
15
                                               dx[id].jp.x[ij] = xx;
                                               dx[id].score = delx;
                                      else {
                                               coll[yy] \approx dely[yy];
20
                                               ij = dx(id).ijmp;
                    if (dx[id].jp.n[0] && (!dna | | (ndely[yy] > = MAXJMP)
                                               && xx > dx[id].jp.x[ij]+MX) \mid mis > dx[id].score+DINS0)) {
                                                         dx[id].ijmp++;
                                                         if (++ij > = MAXJMP) {
25
                                                                  writejmps(id);
                                                                  ij = dx[id].ijmp = 0;
                                                                  dx[id].offset = offset;
                                                                  offset += sizeof(struct jmp) + sizeof(offset);
                                                         }
30
                                               dx[id].jp.n[ij] = -ndely[yy];
                                               dx[id].jp.x[ij] = xx;
                                               dx[id].score = dely[yy];
35
                                      if (xx = = len0 && yy < len1) {
                                               /* last col
                                               if (endgaps)
                                                         coll[yy] = ins0 + ins1*(len1-yy);
40
                                               if (coll[yy] > smax) {
                                                         smax = coll[yy];
                                                         dmax = id;
                                               }
                                      }
45
                             if (endgaps && xx < len0)
                                      col1[yy-1] = ins0 + ins1*(len0-xx);
                             if (coll[yy-1] > smax) {
                                      smax = coll[yy-1];
50
                                      dmax = id:
                             tmp = col0; col0 = col1; col1 = tmp;
                                                                     . }
                    (void) free((char *)ndely);
                    (void) free((char *)dely);
55
                    (void) free((char *)col0);
                    (void) free((char *)col1);
                                                                  }
```

```
print() -- only routine visible outside this module
 5
           * getmat() -- trace back best path, count matches: print()
           * pr_align() -- print alignment of described in array p[]: print()
           * dumpblock() -- dump a block of lines with numbers, stars: pr align()
           * nums() -- put out a number line: dumpblock()
10
           * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
           * stars() - -put a line of stars: dumpblock()
           * stripname() -- strip any path and prefix from a segname
15
           #include "nw.h"
           #define SPC
                              256
           #define P LINE
                                        /* maximum output line */
           #define P_SPC
                              3
                                        /* space between name or num and seq */
20
           extern
                     _day[26][26];
           int
                     olen;
                                        /* set output line length */
           FILE
                     *fx;
                                        /* output file */
25
           print()
                                                                                                                            print
           {
                     int
                              lx, ly, firstgap, lastgap;
                                                           /* overlap */
                     if ((fx = fopen(ofile, "w")) == 0) {
30
                              fprintf(stderr, "%s: can't write %s\n", prog, ofile);
                              cleanup(1);
                     fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
                     fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
35
                     olen = 60;
                     1x = 1en0;
                     ly = len1;
                     firstgap = lastgap = 0;
                     if (dmax < len1 - 1) {
                                                 /* leading gap in x */
40
                              pp[0].spc = firstgap = len1 - dmax - 1;
                              ly -= pp[0].spc;
                     else if (dmax > len1 - 1) { /* leading gap in y */
                              pp[1].spc = firstgap = dmax - (len1 - 1);
45
                              lx -= pp[1].spc;
                     if (dmax0 < len0 - 1) {
                                                 /* trailing gap in x */
                              lastgap = len0 - dmax0 - 1;
                              lx -= lastgap;
50
                     }
                     else if (dmax0 > len0 - 1) { /* trailing gap in y */
                              lastgap = dmax0 - (len0 - 1);
                              ly -= lastgap;
55
                     getmat(lx, ly, firstgap, lastgap);
                     pr_align();
```

```
* trace back the best path, count matches
            */
           static
  5
           getmat(lx, ly, firstgap, lastgap)
                                                                                                                     getmat
                     int
                              lx, ly;
                                                          /* "core" (minus endgaps) */
                     int
                              firstgap, lastgap;
                                                          /* leading trailing overlap */
           {
                     int
                                       nm, i0, i1, siz0, siz1;
 10
                     char
                                       outx[32];
                     double
                                       pct;
                     register
                                       n0, n1;
                     register char
                                       *p0, *p1;
                     /* get total matches, score
 15
                     i0 = i1 = siz0 = siz1 = 0;
                     p0 = seqx[0] + pp[1].spc;
                     p1 = seqx[1] + pp[0].spc;
                     n0 = pp[1].spc + 1;
20
                     n1 = pp[0].spc + 1;
                     nm = 0;
                     while ( *p0 && *p1 ) {
                              if (siz0) {
                                       p1++;
25
                                       n1++;
                                       siz0--;
                              else if (siz1) {
                                       p0++;
30
                                       n0++;
                                       siz1--;
                              else {
                                       if (xbm[*p0-'A']&xbm[*p1-'A'])
35
                                                nm++;
                                       if (n0++==pp[0].x[i0])
                                                siz0 = pp[0].n[i0++];
                                       if (n1++==pp[1].x[i1])
                                                siz1 = pp[1].n[i1++];
40
                                       p0++;
                                       p1++;
                             }
                    }
45
                    /* pct homology:
                     * if penalizing endgaps, base is the shorter seq
                     * else, knock off overhangs and take shorter core
                     */
                    if (endgaps)
50
                             lx = (len0 < len1)? len0 : len1;
                    else
                             lx = (lx < ly)? lx : ly;
                    pct = 100.*(double)nm/(double)lx;
                    fprintf(fx, "\n");
55
                    fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
                             nm, (nm == 1)? "": "es", lx, pct);
```

```
fprintf(fx, " < gaps in first sequence: %d", gapx);
                                                                                                                          ...getmat
                     if (gapx) {
                               (void) sprintf(outx, " (%d %s%s)",
                                         ngapx, (dna)? "base": "residue", (ngapx = = 1)? "": "s");
 5
                               fprintf(fx,"%s", outx);
                     fprintf(fx, ", gaps in second sequence: %d", gapy);
                     if (gapy) {
                               (void) sprintf(outx, " (%d %s%s)",
                                         ngapy, (dna)? "base": "residue", (ngapy == 1)? "": "s");
10
                               fprintf(fx, "%s", outx);
                     if (dna)
                               fprintf(fx,
                               "\n < score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
15
                               smax, DMAT, DMIS, DINSO, DINS1);
                     else
                               "\n < score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
                               smax, PINSO, PINS1);
20
                     if (endgaps)
                               fprintf(fx,
                               "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
                               firstgap, (dna)? "base": "residue", (firstgap == 1)? "": "s", lastgap, (dna)? "base": "residue", (lastgap == 1)? "": "s");
25
                     else
                               fprintf(fx, "<endgaps not penalized\n");</pre>
           }
            static
                               nm;
                                                   /* matches in core - for checking */
            static
                               lmax;
                                                   /* lengths of stripped file names */
30
            static
                               ij[2];
                                                   /* jmp index for a path */
            static
                               nc[2];
                                                   /* number at start of current line */
            static
                                                   /* current elem number -- for gapping */
                               ni[2];
            static
                               siz[2];
            static char
                               *ps[2];
                                                   /* ptr to current element */
35
            static char
                               *po[2];
                                                   /* ptr to next output char slot */
            static char
                               out[2][P_LINE];
                                                   /* output line */
            static char
                               star[P_LINE];
                                                   /* set by stars() */
            * print alignment of described in struct path pp[]
40
           static
           pr_align()
                                                                                                                           pr align
           {
                     int
                                         nn;
                                                   /* char count */
45
                     int
                                         more;
                     register
                                         i;
                     for (i = 0, lmax = 0; i < 2; i++)
                               nn = stripname(namex[i]);
50
                               if (nn > lmax)
                                         lmax = nn;
                               nc[i] = 1;
                               ni[i] = 1;
                               siz[i] = ij[i] = 0;
55
                               ps[i] = seqx[i];
                               po[i] = out[i];
                                                                       }
```

```
for (nn = nm = 0, more = 1; more;)
                                                                                                           ...pr_align
                            for (i = more = 0; i < 2; i++)
  5
                                      * do we have more of this sequence?
                                     if (!*ps[i])
                                              continue;
                                     more++;
10
                                     if (pp[i].spc) {
                                                     /* leading space */
                                              *po[i]++ = ' ';
                                              pp[i].spc--;
                                     }
                                     15
                                              *po[i] + + = '-';
                                              siz[i]--;
                                     }
                                     else {
                                                       /* we're putting a seq element
20
                                              po[i] = ps[i];
                                              if (islower(*ps[i]))
                                                       *ps[i] = toupper(*ps[i]);
                                              po[i]++;
                                              ps[i]++;
25
                                              /*
                                               * are we at next gap for this seq?
                                              if (ni[i] = = pp[i].x[ij[i]]) {
30
                                                       * we need to merge all gaps
                                                       * at this location
                                                       siz[i] = pp[i].n[ij[i]++];
                                                       while (ni[i] = pp[i].x[ij[i]])
35
                                                                siz[i] += pp[i].n[ij[i]++];
                                              ni[i]++;
40
                            if (++nn == olen | | !more && nn) {
                                     dumpblock();
                                     for (i = 0; i < 2; i++)
                                             po[i] = out[i];
                                     nn = 0;
45
                            }
                   }
           * dump a block of lines, including numbers, stars: pr_align()
50
           */
          static
          dumpblock()
                                                                                                          dumpblock
                   register i;
55
                   for (i = 0; i < 2; i++)
                            *po[i]-= '\0';
```

```
...dumpblock
```

```
(void) putc('\n', fx);
                     for (i = 0; i < 2; i++)
                               if (*out[i] && (*out[i] != ' ' | | *(po[i]) != ' ')) {
 5
                                         if (i == 0)
                                                   nums(i);
                                         if (i == 0 && *out[1])
                                                   stars();
                                         putline(i);
10
                                         if (i == 0 && *out[1])
                                                   fprintf(fx, star);
                                         if (i == 1)
                                                   nums(i);
                               }
15
                     }
           }
            * put out a number line: dumpblock()
            */
20
           static
                                                                                                                                nums
           nums(ix)
                     int
                                         /* index in out[] holding seq line */
           {
                     char
                                         nline[P_LINE];
25
                     register
                                         i, j;
                     register char
                                          *pn, *px, *py;
                     for (pn = nline, i = 0; i < lmax+P SPC; i++, pn++)
                               *pn = ' ';
                     for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
    if (*py == ' ' | | *py == '-')
        *pn = ' ';
30
                               else {
                                          if (i\%10 == 0 | | (i == 1 \&\& nc[ix] != 1)) {
                                                    j = (i < 0)? -i : i;
35
                                                    for (px = pn; j; j /= 10, px-)
                                                              *px = j\%10 + '0';
                                                    if (i < 0)
                                                              *px = '-';
                                          }
40
                                          else
                                                    *pn = ' ';
                                          i++;
                               }
45
                      *pn = '0';
                     nc[ix] = i;
                     for (pn = nline; *pn; pn++)
                                (void) putc(*pn, fx);
                      (void) putc('\n', fx);
50
             * put out a line (name, [num], seq, [num]): dumpblock()
            static
                                                                                                                              putline
55
            putline(ix)
                                                              {
                      int
                                ix;
```

```
...putline
                    int
                                        i;
                                        *px;
                    register char
 5
                    for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
                              (void) putc(*px, fx);
                    for (; i < lmax + P_SPC; i++)
                              (void) putc(' ', fx);
10
                    /* these count from 1:
                     * ni[] is current element (from 1)
                     * nc[] is number at start of current line
15
                     for (px = out[ix]; *px; px++)
                               (void) putc(*px&0x7F, fx);
                     (void) putc('\n', fx);
          }
20
           * put a line of stars (seqs always in out[0], out[1]): dumpblock()
           static
                                                                                                                              stars
25
           stars()
           {
                                         *p0, *p1, cx, *px;
                     register char
                     if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
!*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
30
                               return;
                     px = star;
                     for (i = lmax + P_SPC; i; i--)
35
                               *px++ = ' ';
                     for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
                               if (isalpha(*p0) && isalpha(*p1)) {
40
                                         if (xbm[*p0-'A']&xbm[*p1-'A']) {
                                                   cx = '*';
                                                   nm++;
                                         }
                                         else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
45
                                                   cx = '.\ddot{};
                                         else
                                                   cx = ' ';
                               }
                               else
50
                                         cx = ' ';
                               *px++ = cx;
                      *px++ = '\n';
                     *px = '0';
55
           }
```

stripname

```
* strip path or prefix from pn, return len: pr_align()
            */
           static
 5
           stripname(pn)
                               *pn;
                                         /* file name (may be path) */
           {
                     register char
                                         *px, *py;
10
                     py = 0;
                     for (px = pn; *px; px + +)
if (*px == '/')
                                         py = px + 1;
                     if (py)
15
                               (void) strcpy(pn, py);
                     return(strlen(pn));
           }
20
```

```
* cleanup() -- cleanup any tmp file
           * getseq() -- read in seq, set dna, len, maxlen
           * g calloc() -- calloc() with error checkin
 5
           * readjmps() - get the good jmps, from tmp file if necessary
           * writejmps() -- write a filled array of jmps to a tmp file: nw()
          #include "nw.h"
          #include < sys/file.h>
10
                                                                    /* tmp file for jmps */
                    *jname = "/tmp/homgXXXXXX";
          char
                    *fj;
          FILE
                                                                     /* cleanup tmp file */
          int
                    cleanup();
          long
                    Iseek();
15
           * remove any tmp file if we blow
           */
                                                                                                                        cleanup
           cleanup(i)
                              i;
                    int
20
                     if (fj)
                              (void) unlink(jname);
                     exit(i);
25
            * read, return ptr to seq, set dna, len, maxlen
            * skip lines starting with ';', '<', or '>'
            * seq in upper or lower case
            */
30
           char
                                                                                                                           getseq
           getseq(file, len)
                     char
                               *file:
                                        /* file name */
                     int
                               *len;
                                        /* seq len */
           {
35
                                        line[1024], *pseq;
                     char
                     register char
                                         *px, *py;
                                        natgo, tlen;
                     int
                     FILE
                                         *fp;
                     if ((fp = fopen(file, "r")) == 0) {
                               fprintf(stderr, "%s: can't read %s\n", prog, file);
40
                               exit(1);
                     }
                     tlen = natgc = 0;
                     while (fgets(line, 1024, fp)) {
45
                               if (*line == ';' | | *line == '<' | | *line == '>')
                                         continue;
                               for (px = line; *px != '\n'; px++)
                                         if (isupper(*px) | | islower(*px))
                                                  tlen++;
50
                     if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
                               fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
                               exit(1);
 55
                     pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
```

```
...getseq
                    py = pseq + 4;
                    *len = tlen;
                    rewind(fp);
 5
                    while (fgets(line, 1024, fp)) {
                             if (*line == ';' || *line == '<' || *line == '>')
                                      continue;
                             for (px = line; *px != '\n'; px++) {
                                      if (isupper(*px))
10
                                               *py++ = *px;
                                      else if (islower(*px))
                                               *py++ = toupper(*px);
                                      if (index("ATGCU",*(py-1)))
                                               natgc++;
15
                             }
                    *py++ = '\0';
                    *py = '\0';
                    (void) fclose(fp);
20
                    dna = natgc > (tlen/3);
                    return(pseq+4);
          }
          char
          g_calloc(msg, nx, sz)
                                                                                                                   g_calloc
25
                    char
                             *msg;
                                               /* program, calling routine */
                    int
                                               /* number and size of elements */
                             nx, sz;
          {
                    char
                                       *px, *calloc();
                    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
30
                             if (*msg) {
                                       fprintf(stderr, "%s: g_calloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
                             }
35
                    return(px);
          }
           * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
40
          readjmps()
                                                                                                                 readjmps
          {
                    int
                                      fd = -1;
                                      siz, i0, i1;
45
                    register i, j, xx;
                    if (fj) {
                             (void) fclose(fj);
                             if ((fd = open(jname, O_RDONLY, 0)) < 0) {
                                       fprintf(stderr, "%s: can't open() %s\n", prog, jname);
50
                                      cleanup(1);
                             }
                    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
                             while (1) {
55
                                      for (j = dx[dmax].ijmp; j > = 0 && dx[dmax].jp.x[j] > = xx; j-)
```

```
...readjmps
                                         if (j < 0 \&\& dx[dmax].offset \&\& fj) {
                                                   (void) lseek(fd, dx[dmax].offset, 0);
                                                   (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
  5
                                                   (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
                                                   dx[dmax].ijmp = MAXJMP-1:
                                         else
                                                  break;
                               if (i > = JMPS) {
10
                                         fprintf(stderr, "%s: too many gaps in alignment\n", prog);
                                         cleanup(1);
                               if (j > = 0) {
                                         siz = dx[dmax].jp.n[j];
15
                                         xx = dx[dmax].jp.x[j];
                                         dmax += siz;
                                         if (siz < 0) {
                                                                      /* gap in second seq */
                                                   pp[1].n[i1] = -siz;
                                                   xx += siz;
20
                                                   /* id = xx - yy + len1 - 1
                                                                                                              */
                                                  pp[1].x[i1] = xx - dmax + len1 - 1;
                                                  gapy++;
                                                  ngapy -= siz;
           /* ignore MAXGAP when doing endgaps */
25
                                                   siz = (-siz < MAXGAP | | endgaps)? -siz : MAXGAP;
                                                  i1++;
                                         else if (siz > 0) { /* gap in first seq */
                                                  pp[0].n[i0] = siz;
30
                                                  pp[0].x[i0] = xx;
                                                  gapx++;
                                                  ngapx += siz;
           /* ignore MAXGAP when doing endgaps */
                                                   siz = (siz < MAXGAP | | endgaps)? siz : MAXGAP;
35
                                         }
                               else
                                         break;
40
                     /* reverse the order of jmps */
                     for (j = 0, i0-; j < i0; j++, i0--) {
                               i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
                               i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
45
                     for (j = 0, i1-; j < i1; j++, i1-)
                              i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;

i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
50
                     if (fd > = 0)
                               (void) close(fd);
                     if (fj) {
                               (void) unlink(jname);
                               fi = 0:
55
                               offset = 0;
                    }
                                                            }
```

```
* write a filled jmp struct offset of the prev one (if any): nw()
  5
               writejmps(ix)
                                                                                                                                                                  writejmps
                             int
                                          *mktemp();
                             char
10
                             if (!fj) {
                                          if (mktemp(jname) < 0) {
     fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);</pre>
                                                        cleanup(1);

}
if ((fj = fopen(jname, "w")) == 0) {
    fprintf(stderr, "%s: can't write %s\n", prog, jname);
    exit(1);

15
                            }
(void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
(void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
20
               }
```

Table 2

TAT

XXXXXXXXXXXXX

(Length = 15 amino acids)

Comparison Protein

XXXXXYYYYYYY

(Length = 12 amino acids)

5 % amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the TAT polypeptide) =

10 5 divided by 15 = 33.3%

Table 3

TAT

XXXXXXXXX

(Length = 10 amino acids)

15 Comparison Protein

XXXXXYYYYYYZZYZ

(Length = 15 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the TAT polypeptide) =

5 divided by 10 = 50%

Table 4

25

20

TAT-DNA

NNNNNNNNNNN

(Length = 14 nucleotides)

Comparison DNA

NNNNNLLLLLLLLL

(Length = 16 nucleotides)

% nucleic acid sequence identity =

30

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the TAT-DNA nucleic acid sequence) = 6 divided by 14 = 42.9%

Table 5

TAT-DNA

NNNNNNNNNNN

(Length = 12 nucleotides)

Comparison DNA

NNNNLLLVV

(Length = 9 nucleotides)

5 % nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the TAT-DNA nucleic acid sequence) =

10 4 divided by 12 = 33.3%

15

20

25

30

35

II. Compositions and Methods of the Invention

A. Anti-TAT Antibodies

In one embodiment, the present invention provides anti-TAT antibodies which may find use herein as therapeutic and/or diagnostic agents. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

Polyclonal antibodies are preferably raised in animals by multiple subcutaneous (sc) or intraperitoneal (ip) injections of the relevant antigen and an adjuvant. It may be useful to conjugate the relevant antigen (especially when synthetic peptides are used) to a protein that is immunogenic in the species to be immunized. For example, the antigen can be conjugated to keyhole limpet hemocyanin (KLH), serum albumin, bovine thyroglobulin, or soybean trypsin inhibitor, using a bifunctional or derivatizing agent, e.g., maleimidobenzoyl sulfosuccinimide ester (conjugation through cysteine residues), N-hydroxysuccinimide (through lysine residues), glutaraldehyde, succinic anhydride, SOCl₂, or R¹N=C=NR, where R and R¹ are different alkyl groups.

Animals are immunized against the antigen, immunogenic conjugates, or derivatives by combining, e.g., 100 µg or 5 µg of the protein or conjugate (for rabbits or mice, respectively) with 3 volumes of Freund's complete adjuvant and injecting the solution intradermally at multiple sites. One month later, the animals are boosted with 1/5 to 1/10 the original amount of peptide or conjugate in Freund's complete adjuvant by subcutaneous injection at multiple sites. Seven to 14 days later, the animals are bled and the serum is assayed for antibody titer. Animals are boosted until the titer plateaus. Conjugates also can be made in recombinant cell culture as protein fusions. Also, aggregating agents such as alum are suitably used to enhance the immune response.

2. Monoclonal Antibodies

Monoclonal antibodies may be made using the hybridoma method first described by Kohler et al., Nature, 256:495 (1975), or may be made by recombinant DNA methods (U.S. Patent No. 4,816,567).

In the hybridoma method, a mouse or other appropriate host animal, such as a hamster, is immunized

as described above to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the protein used for immunization. Alternatively, lymphocytes may be immunized *in vitro*. After immunization, lymphocytes are isolated and then fused with a myeloma cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, pp.59-103 (Academic Press, 1986)).

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The hybridoma cells thus prepared are seeded and grown in a suitable culture medium which medium preferably contains one or more substances that inhibit the growth or survival of the unfused, parental myeloma cells (also referred to as fusion partner). For example, if the parental myeloma cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the selective culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine (HAT medium), which substances prevent the growth of HGPRT-deficient cells.

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Preferred fusion partner myeloma cells are those that fuse efficiently, support stable high-level production of antibody by the selected antibody-producing cells, and are sensitive to a selective medium that selects against the unfused parental cells. Preferred myeloma cell lines are murine myeloma lines, such as those derived from MOPC-21 and MPC-11 mouse tumors available from the Salk Institute Cell Distribution Center, San Diego, California USA, and SP-2 and derivatives e.g., X63-Ag8-653 cells available from the American Type Culture Collection, Manassas, Virginia, USA. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); and Brodeur et al., Monoclonal Antibody Production Techniques and Applications, pp. 51-63 (Marcel Dekker, Inc., New York, 1987)).

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Culture medium in which hybridoma cells are growing is assayed for production of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunosorbent assay (ELISA).

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The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis described in Munson et al., <u>Anal. Biochem.</u>, 107:220 (1980).

Once hybridoma cells that produce antibodies of the desired specificity, affinity, and/or activity are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods (Goding, Monoclonal Antibodies: Principles and Practice, pp.59-103 (Academic Press, 1986)). Suitable culture media for this purpose include, for example, D-MEM or RPMI-1640 medium. In addition, the hybridoma cells may be grown *in vivo* as ascites tumors in an animal e.g., by i.p. injection of the cells into mice.

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The monoclonal antibodies secreted by the subclones are suitably separated from the culture medium, ascites fluid, or serum by conventional antibody purification procedures such as, for example, affinity chromatography (e.g., using protein A or protein G-Sepharose) or ion-exchange chromatography, hydroxylapatite chromatography, gel electrophoresis, dialysis, etc.

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DNA encoding the monoclonal antibodies is readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the

heavy and light chains of murine antibodies). The hybridoma cells serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as *E. coli* cells, simian COS cells, Chinese Hamster Ovary (CHO) cells, or myeloma cells that do not otherwise produce antibody protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. Review articles on recombinant expression in bacteria of DNA encoding the antibody include Skerra et al., <u>Curr. Opinion in Immunol.</u>, 5:256-262 (1993) and Plückthun, <u>Immunol. Revs.</u> 130:151-188 (1992).

In a further embodiment, monoclonal antibodies or antibody fragments can be isolated from antibody phage libraries generated using the techniques described in McCafferty et al., Nature, 348:552-554 (1990). Clackson et al., Nature, 352:624-628 (1991) and Marks et al., J. Mol. Biol., 222:581-597 (1991) describe the isolation of murine and human antibodies, respectively, using phage libraries. Subsequent publications describe the production of high affinity (nM range) human antibodies by chain shuffling (Marks et al., Bio/Technology, 10:779-783 (1992)), as well as combinatorial infection and *in vivo* recombination as a strategy for constructing very large phage libraries (Waterhouse et al., Nuc. Acids. Res. 21:2265-2266 (1993)). Thus, these techniques are viable alternatives to traditional monoclonal antibody hybridoma techniques for isolation of monoclonal antibodies.

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The DNA that encodes the antibody may be modified to produce chimeric or fusion antibody polypeptides, for example, by substituting human heavy chain and light chain constant domain (C _H and C_L) sequences for the homologous murine sequences (U.S. Patent No. 4,816,567; and Morrison, et al., <u>Proc. Natl Acad. Sci. USA</u>, 81:6851 (1984)), or by fusing the immunoglobulin coding sequence with all or part of the coding sequence for a non-immunoglobulin polypeptide (heterologous polypeptide). The non-immunoglobulin polypeptide sequences can substitute for the constant domains of an antibody, or they are substituted for the variable domains of one antigen-combining site of an antibody to create a chimeric bivalent antibody comprising one antigen-combining site having specificity for an antigen and another antigen-combining site having specificity for a different antigen.

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3. Human and Humanized Antibodies

The anti-TAT antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab') 2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the FR regions are

those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

The choice of human variable domains, both light and heavy, to be used in making the humanized antibodies is very important to reduce antigenicity and HAMA response (human anti-mouse antibody) when the antibody is intended for human therapeutic use. According to the so-called "best-fit" method, the sequence of the variable domain of a rodent antibody is screened against the entire library of known human variable domain sequences. The human V domain sequence which is closest to that of the rodent is identified and the human framework region (FR) within it accepted for the humanized antibody (Sims et al., J. Immunol. 151:2296 (1993); Chothia et al., J. Mol. Biol., 196:901 (1987)). Another method uses a particular framework region derived from the consensus sequence of all human antibodies of a particular subgroup of light or heavy chains. The same framework may be used for several different humanized antibodies (Carter et al., Proc. Natl. Acad. Sci. USA, 89:4285 (1992); Presta et al., J. Immunol. 151:2623 (1993)).

It is further important that antibodies be humanized with retention of high binding affinity for the antigen and other favorable biological properties. To achieve this goal, according to a preferred method, humanized antibodies are prepared by a process of analysis of the parental sequences and various conceptual humanized products using three-dimensional models of the parental and humanized sequences. Three-dimensional immunoglobulin models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate immunoglobulin sequences. Inspection of these displays permits analysis of the likely role of the residues in the functioning of the candidate immunoglobulin sequence, i.e., the analysis of residues that influence the ability of the candidate immunoglobulin to bind its antigen. In this way, FR residues can be selected and combined from the recipient and import sequences so that the desired antibody characteristic, such as increased affinity for the target antigen(s), is achieved. In general, the hypervariable region residues are directly and most substantially involved in influencing antigen binding.

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Various forms of a humanized anti-TAT antibody are contemplated. For example, the humanized antibody may be an antibody fragment, such as a Fab, which is optionally conjugated with one or more cytotoxic agent(s) in order to generate an immunoconjugate. Alternatively, the humanized antibody may be an intact antibody, such as an intact IgG1 antibody.

As an alternative to humanization, human antibodies can be generated. For example, it is now possible to produce transgenic animals (e.g., mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production. For example, it has been described that the homozygous deletion of the antibody heavy-chain joining region (J_H) gene in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array into such germ-line mutant mice will result in the production of human antibodies upon antigen challenge. See, e.g., Jakobovits et al., Proc. Natl. Acad. Sci. USA, 90:2551 (1993); Jakobovits et al., Nature, 362:255-258 (1993); Bruggemann et al., Year in Immuno. 7:33 (1993); U.S. Patent Nos. 5,545,806, 5,569,825, 5,591,669 (all of GenPharm); 5,545,807; and WO 97/17852.

Alternatively, phage display technology (McCafferty et al., Nature 348:552-553 [1990]) can be used to produce human antibodies and antibody fragments in vitro, from immunoglobulin variable (V) domain gene repertoires from unimmunized donors. According to this technique, antibody V domain genes are cloned inframe into either a major or minor coat protein gene of a filamentous bacteriophage, such as M13 or fd, and displayed as functional antibody fragments on the surface of the phage particle. Because the filamentous particle contains a single-stranded DNA copy of the phage genome, selections based on the functional properties of the antibody also result in selection of the gene encoding the antibody exhibiting those properties. Thus, the phage mimics some of the properties of the B-cell. Phage display can be performed in a variety of formats, reviewed in, e.g., Johnson, Kevin S. and Chiswell, David J., Current Opinion in Structural Biology 3:564-571 (1993). Several sources of V-gene segments can be used for phage display. Clackson et al. Nature, 352:624-628 (1991) isolated a diverse array of anti-oxazolone antibodies from a small random combinatorial library of V genes derived from the spleens of immunized mice. A repertoire of V genes from unimmunized human donors can be constructed and antibodies to a diverse array of antigens (including self-antigens) can be isolated essentially following the techniques described by Marks et al., J. Mol. Biol. 222:581-597 (1991), or Griffith et al., EMBO J. 12:725-734 (1993). See, also, U.S. Patent Nos. 5,565,332 and 5,573,905.

As discussed above, human antibodies may also be generated by *in vitro* activated B cells (see U.S. Patents 5,567,610 and 5,229,275).

4. Antibody fragments

In certain circumstances there are advantages of using antibody fragments, rather than whole antibodies. The smaller size of the fragments allows for rapid clearance, and may lead to improved access to solid tumors.

Various techniques have been developed for the production of antibody fragments. Traditionally, these fragments were derived via proteolytic digestion of intact antibodies (see, e.g., Morimoto et al., <u>Journal of Biochemical and Biophysical Methods</u> 24:107-117 (1992); and Brennan et al., <u>Science</u>, 229:81 (1985)).

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F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent, sodium arsenite, to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Recent progress has facilitated the direct recovery of Fab'-SH fragments from E. coli, which can be chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175: 217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol., 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a V_H connected to a V_L by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See Gruber et al., J. Immunol., 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., <u>J. Immunol.</u> 147:60 (1991).

6. <u>Heteroconjugate Antibodies</u>

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

7. <u>Multivalent Antibodies</u>

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A multivalent antibody may be internalized (and/or catabolized) faster than a bivalent antibody by a cell expressing an antigen to which the antibodies bind. The antibodies of the present invention can be multivalent antibodies (which are other than of the IgM class) with three or more antigen binding sites (e.g. tetravalent antibodies), which can be readily produced by recombinant expression of nucleic acid encoding the polypeptide chains of the antibody. The multivalent antibody can comprise a dimerization domain and three or more antigen binding sites. The preferred dimerization domain comprises (or consists of) an Fc region or a hinge region. In this scenario, the antibody will comprise an Fc region and three or more antigen binding sites amino-terminal to the Fc region. The preferred multivalent antibody herein comprises (or consists of) three to about eight, but preferably four, antigen binding sites. The multivalent antibody comprises at least one polypeptide chain (and preferably two polypeptide chains), wherein the polypeptide chain(s) comprise two or more variable domains. For instance, the polypeptide chain(s) may comprise VD1-(X1) __n-VD2-(X2)_n-Fc, wherein VD1 is a first variable domain, VD2 is a second variable domain, Fc is one polypeptide chain of an Fc region, X1 and X2 represent an amino acid or polypeptide, and n is 0 or 1. For instance, the polypeptide chain(s) may comprise: VH-CH1-flexible linker-VH-CH1-Fc region chain; or VH-CH1-VH-CH1-Fc region chain. The multivalent antibody herein preferably further comprises at least two (and preferably four) light chain variable domain polypeptides. The multivalent antibody herein may, for instance, comprise from about two to about eight light chain variable domain polypeptides. The light chain variable domain polypeptides contemplated here comprise a light chain variable domain and, optionally, further comprise a CL domain.

8. Effector Function Engineering

It may be desirable to modify the antibody of the invention with respect to effector function, e.g., so as to enhance antigen-dependent cell-mediated cyotoxicity (ADCC) and/or complement dependent cytotoxicity (CDC) of the antibody. This may be achieved by introducing one or more amino acid substitutions in an Fc region of the antibody. Alternatively or additionally, cysteine residue(s) may be introduced in the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med. 176:1191-1195 (1992) and Shopes, B. J. Immunol. 148:2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff et al., Cancer Research 53:2560-2565 (1993). Alternatively, an antibody can be engineered which has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design 3:219-230 (1989).

To increase the serum half life of the antibody, one may incorporate a salvage receptor binding epitope into the antibody (especially an antibody fragment) as described in U.S. Patent 5,739,277, for example. As used herein, the term "salvage receptor binding epitope" refers to an epitope of the Fc region of an IgG molecule (e.g., IgG₁, IgG₂, IgG₃, or IgG₄) that is responsible for increasing the *in vivo* serum half-life of the IgG molecule.

9. <u>Immunoconjugates</u>

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic

agent such as a chemotherapeutic agent, a growth inhibitory agent, a toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include 212Bi, 131I, ¹³¹In, ⁹⁰Y, and ¹⁸⁶Re. Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

Conjugates of an antibody and one or more small molecule toxins, such as a calicheamicin, maytansinoids, a trichothene, and CC1065, and the derivatives of these toxins that have toxin activity, are also contemplated herein.

Maytansine and maytansinoids

In one preferred embodiment, an anti-TAT antibody (full length or fragments) of the invention is conjugated to one or more maytansinoid molecules.

Maytansinoids are mitototic inhibitors which act by inhibiting tubulin polymerization. Maytansine was first isolated from the east African shrub *Maytenus serrata* (U.S. Patent No. 3,896,111). Subsequently, it was discovered that certain microbes also produce maytansinoids, such as maytansinol and C-3 maytansinol esters (U.S. Patent No. 4,151,042). Synthetic maytansinol and derivatives and analogues thereof are disclosed, for example, in U.S. Patent Nos. 4,137,230; 4,248,870; 4,256,746; 4,260,608; 4,265,814; 4,294,757; 4,307,016; 4,308,268; 4,308,269; 4,309,428; 4,313,946; 4,315,929; 4,317,821; 4,322,348; 4,331,598; 4,361,650; 4,364,866; 4,424,219; 4,450,254; 4,362,663; and 4,371,533, the disclosures of which are hereby expressly incorporated by reference.

Maytansinoid-antibody conjugates

In an attempt to improve their therapeutic index, maytansine and maytansinoids have been conjugated to antibodies specifically binding to tumor cell antigens. Immunoconjugates containing maytansinoids and their therapeutic use are disclosed, for example, in U.S. Patent Nos. 5,208,020, 5,416,064 and European Patent EP

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0 425 235 B1, the disclosures of which are hereby expressly incorporated by reference. Liu et al., <u>Proc. Natl. Acad. Sci. USA</u> 93:8618-8623 (1996) described immunoconjugates comprising a maytansinoid designated DM1 linked to the monoclonal antibody C242 directed against human colorectal cancer. The conjugate was found to be highly cytotoxic towards cultured colon cancer cells, and showed antitumor activity in an *in vivo* tumor growth assay. Chari et al., <u>Cancer Research</u> 52:127-131 (1992) describe immunoconjugates in which a maytansinoid was conjugated via a disulfide linker to the murine antibody A7 binding to an antigen on human colon cancer cell lines, or to another murine monoclonal antibody TA.1 that binds the HER-2/neu oncogene. The cytotoxicity of the TA.1-maytansonoid conjugate was tested *in vitro* on the human breast cancer cell line SK-BR-3, which expresses 3 x 10⁵ HER-2 surface antigens per cell. The drug conjugate achieved a degree of cytotoxicity similar to the free maytansonid drug, which could be increased by increasing the number of maytansinoid molecules per antibody molecule. The A7-maytansinoid conjugate showed low systemic cytotoxicity in mice.

Anti-TAT polypeptide antibody-maytansinoid conjugates (immunoconjugates)

Anti-TAT antibody-maytansinoid conjugates are prepared by chemically linking an anti-TAT antibody to a maytansinoid molecule without significantly diminishing the biological activity of either the antibody or the maytansinoid molecule. An average of 3-4 maytansinoid molecules conjugated per antibody molecule has shown efficacy in enhancing cytotoxicity of target cells without negatively affecting the function or solubility of the antibody, although even one molecule of toxin/antibody would be expected to enhance cytotoxicity over the use of naked antibody. Maytansinoids are well known in the art and can be synthesized by known techniques or isolated from natural sources. Suitable maytansinoids are disclosed, for example, in U.S. Patent No. 5,208,020 and in the other patents and nonpatent publications referred to hereinabove. Preferred maytansinoids are maytansinol and maytansinol analogues modified in the aromatic ring or at other positions of the maytansinol molecule, such as various maytansinol esters.

There are many linking groups known in the art for making antibody-maytansinoid conjugates, including, for example, those disclosed in U.S. Patent No. 5,208,020 or EP Patent 0 425 235 B1, and Chari et al., <u>Cancer Research</u> 52:127-131 (1992). The linking groups include disufide groups, thioether groups, acid labile groups, photolabile groups, peptidase labile groups, or esterase labile groups, as disclosed in the above-identified patents, disulfide and thioether groups being preferred.

Conjugates of the antibody and maytansinoid may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl) cyclohexane-1-carboxylate, iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as toluene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). Particularly preferred coupling agents include N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP) (Carlsson et al. <u>Biochem. J.</u> 173:723-737 [1978]) and N-succinimidyl-4-(2-pyridylthio)pentanoate (SPP) to provide for a disulfide linkage.

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The linker may be attached to the maytansinoid molecule at various positions, depending on the type of the link. For example, an ester linkage may be formed by reaction with a hydroxyl group using conventional coupling techniques. The reaction may occur at the C-3 position having a hydroxyl group, the C-14 position modified with hyrdoxymethyl, the C-15 position modified with a hydroxyl group, and the C-20 position having a hydroxyl group. In a preferred embodiment, the linkage is formed at the C-3 position of maytansinol or a maytansinol analogue.

Calicheamicin

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Another immunoconjugate of interest comprises an anti-TAT antibody conjugated to one or more calicheamicin molecules. The calicheamicin family of antibiotics are capable of producing double-stranded DNA breaks at sub-picomolar concentrations. For the preparation of conjugates of the calicheamicin family, see U.S. patents 5,712,374, 5,714,586, 5,739,116, 5,767,285, 5,770,701, 5,770,710, 5,773,001, 5,877,296 (all to American Cyanamid Company). Structural analogues of calicheamicin which may be used include, but are not limited to, γ_1^I , α_2^I , α_3^I , N-acetyl- γ_1^I , PSAG and θ_1^I (Hinman et al., Cancer Research 53:3336-3342 (1993), Lode et al., Cancer Research 58:2925-2928 (1998) and the aforementioned U.S. patents to American Cyanamid). Another anti-tumor drug that the antibody can be conjugated is QFA which is an antifolate. Both calicheamicin and QFA have intracellular sites of action and do not readily cross the plasma membrane. Therefore, cellular uptake of these agents through antibody mediated internalization greatly enhances their cytotoxic effects.

Other cytotoxic agents

Other antitumor agents that can be conjugated to the anti-TAT antibodies of the invention include BCNU, streptozoicin, vincristine and 5-fluorouracil, the family of agents known collectively LL-E33288 complex described in U.S. patents 5,053,394, 5,770,710, as well as esperamicins (U.S. patent 5,877,296).

Enzymatically active toxins and fragments thereof which can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin and the tricothecenes. See, for example, WO 93/21232 published October 28, 1993.

The present invention further contemplates an immunoconjugate formed between an antibody and a compound with nucleolytic activity (e.g., a ribonuclease or a DNA endonuclease such as a deoxyribonuclease; DNase).

For selective destruction of the tumor, the antibody may comprise a highly radioactive atom. A variety of radioactive isotopes are available for the production of radioconjugated anti-TAT antibodies. Examples include At²¹¹, I¹³¹, I¹²⁵, Y⁹⁰, Re¹⁸⁶, Re¹⁸⁸, Sm¹⁵³, Bi²¹², P³², Pb²¹² and radioactive isotopes of Lu. When the conjugate is used for diagnosis, it may comprise a radioactive atom for scintigraphic studies, for example tc^{99m} or I¹²³, or a spin label for nuclear magnetic resonance (NMR) imaging (also known as magnetic resonance

imaging, mri), such as iodine-123 again, iodine-131, indium-111, fluorine-19, carbon-13, nitrogen-15, oxygen-17, gadolinium, manganese or iron.

The radio- or other labels may be incorporated in the conjugate in known ways. For example, the peptide may be biosynthesized or may be synthesized by chemical amino acid synthesis using suitable amino acid precursors involving, for example, fluorine-19 in place of hydrogen. Labels such as tc^{99m} or I¹²³, .Re¹⁸⁶, Re¹⁸⁸ and In¹¹¹ can be attached via a cysteine residue in the peptide. Yttrium-90 can be attached via a lysine residue. The IODOGEN method (Fraker et al (1978) Biochem. Biophys. Res. Commun. 80: 49-57 can be used to incorporate iodine-123. "Monoclonal Antibodies in Immunoscintigraphy" (Chatal, CRC Press 1989) describes other methods in detail.

Conjugates of the antibody and cytotoxic agent may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl) cyclohexane-1-carboxylate, iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science 238:1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026. The linker may be a "cleavable linker" facilitating release of the cytotoxic drug in the cell. For example, an acid-labile linker, peptidase-sensitive linker, photolabile linker, dimethyl linker or disulfide-containing linker (Chari et al., Cancer Research 52:127-131 (1992); U.S. Patent No. 5,208,020) may be used.

Alternatively, a fusion protein comprising the anti-TAT antibody and cytotoxic agent may be made, e.g., by recombinant techniques or peptide synthesis. The length of DNA may comprise respective regions encoding the two portions of the conjugate either adjacent one another or separated by a region encoding a linker peptide which does not destroy the desired properties of the conjugate.

In yet another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pre-targeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) which is conjugated to a cytotoxic agent (e.g., a radionucleotide).

10. <u>Immunoliposomes</u>

The anti-TAT antibodies disclosed herein may also be formulated as immunoliposomes. A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein et al., <u>Proc. Natl. Acad. Sci. USA</u> 82:3688 (1985); Hwang et al., <u>Proc. Natl. Acad. Sci. USA</u> 77:4030 (1980); U.S. Pat. Nos. 4,485,045 and 4,544,545;

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and WO97/38731 published October 23, 1997. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin et al., <u>J. Biol. Chem.</u> 257:286-288 (1982) via a disulfide interchange reaction. A chemotherapeutic agent is optionally contained within the liposome. See Gabizon et al., <u>J. National Cancer Inst.</u> 81(19):1484 (1989).

B. TAT Binding Oligopeptides

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TAT binding oligopeptides of the present invention are oligopeptides that bind, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be chemically synthesized using known oligopeptide synthesis methodology or may be prepared and purified using recombinant technology. TAT binding oligopeptides are usually at least about 5 amino acids in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length or more, wherein such oligopeptides that are capable of binding, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening oligopeptide libraries for oligopeptides that are capable of specifically binding to a polypeptide target are well known in the art (see, e.g., U.S. Patent Nos. 5,556,762, 5,750,373, 4,708,871, 4,833,092, 5,223,409, 5,403,484, 5,571,689, 5,663,143; PCT Publication Nos. WO 84/03506 and WO84/03564; Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 81:3998-4002 (1984); Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 82:178-182 (1985); Geysen et al., in Synthetic Peptides as Antigens, 130-149 (1986); Geysen et al., J. Immunol. Meth., 102:259-274 (1987); Schoofs et al., J. Immunol., 140:611-616 (1988), Cwirla, S. E. et al. (1990) Proc. Natl. Acad. Sci. USA, 87:6378; Lowman, H.B. et al. (1991) Biochemistry, 30:10832; Clackson, T. et al. (1991) Nature, 352: 624; Marks, J. D. et al. (1991), J. Mol. Biol., 222:581; Kang, A.S. et al. (1991) Proc. Natl. Acad. Sci. USA, 88:8363, and Smith, G. P. (1991) Current Opin. Biotechnol., 2:668).

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In this regard, bacteriophage (phage) display is one well known technique which allows one to screen large oligopeptide libraries to identify member(s) of those libraries which are capable of specifically binding to a polypeptide target. Phage display is a technique by which variant polypeptides are displayed as fusion proteins to the coat protein on the surface of bacteriophage particles (Scott, J.K. and Smith, G. P. (1990) Science 249: 386). The utility of phage display lies in the fact that large libraries of selectively randomized protein variants (or randomly cloned cDNAs) can be rapidly and efficiently sorted for those sequences that bind to a target molecule with high affinity. Display of peptide (Cwirla, S. E. et al. (1990) Proc. Natl. Acad. Sci.

that are capable of binding, preferably specifically, to a TAT polypeptide as described herein may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening organic molecule libraries for molecules that are capable of binding to a polypeptide target are well known in the art (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585). TAT binding organic molecules may be, for example, aldehydes, ketones, oximes, hydrazones, semicarbazones, carbazides, primary amines, secondary amines, tertiary amines, N-substituted hydrazines, hydrazides, alcohols, ethers, thiols, thioethers, disulfides, carboxylic acids, esters, amides, ureas, carbamates, carbonates, ketals, thioketals, acetals, thioacetals, aryl halides, aryl sulfonates, alkyl halides, alkyl sulfonates, aromatic compounds, heterocyclic compounds, anilines, alkenes, alkynes, diols, amino alcohols, oxazolidines, oxazolines, thiazolidines, thiazolines, enamines, sulfonamides, epoxides, aziridines, isocyanates, sulfonyl chlorides, diazo compounds, acid chlorides, or the like.

D. <u>Screening for Anti-TAT Antibodies, TAT Binding Oligopeptides and TAT Binding Organic</u> <u>Molecules With the Desired Properties</u>

Techniques for generating antibodies, oligopeptides and organic molecules that bind to TAT polypeptides have been described above. One may further select antibodies, oligopeptides or other organic molecules with certain biological characteristics, as desired.

The growth inhibitory effects of an anti-TAT antibody, oligopeptide or other organic molecule of the invention may be assessed by methods known in the art, e.g., using cells which express a TAT polypeptide either endogenously or following transfection with the TAT gene. For example, appropriate tumor cell lines and TAT-transfected cells may treated with an anti-TAT monoclonal antibody, oligopeptide or other organic molecule of the invention at various concentrations for a few days (e.g., 2-7) days and stained with crystal violet or MTT or analyzed by some other colorimetric assay. Another method of measuring proliferation would be by comparing ³H-thymidine uptake by the cells treated in the presence or absence an anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule of the invention. After treatment, the cells are harvested and the amount of radioactivity incorporated into the DNA quantitated in a scintillation counter. Appropriate positive controls include treatment of a selected cell line with a growth inhibitory antibody known to inhibit growth of that cell line. Growth inhibition of tumor cells in vivo can be determined in various ways known in the art. Preferably, the tumor cell is one that overexpresses a TAT polypeptide. Preferably, the anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule will inhibit cell proliferation of a TATexpressing tumor cell in vitro or in vivo by about 25-100% compared to the untreated tumor cell, more preferably, by about 30-100%, and even more preferably by about 50-100% or 70-100%, in one embodiment, at an antibody concentration of about 0.5 to 30 µg/ml. Growth inhibition can be measured at an antibody concentration of about 0.5 to 30 µg/ml or about 0.5 nM to 200 nM in cell culture, where the growth inhibition is determined 1-10 days after exposure of the tumor cells to the antibody. The antibody is growth inhibitory in vivo if administration of the anti-TAT antibody at about 1 µg/kg to about 100 mg/kg body weight results in reduction in tumor size or reduction of tumor cell proliferation within about 5 days to 3 months from the first administration of the antibody, preferably within about 5 to 30 days.

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USA, 87:6378) or protein (Lowman, H.B. et al. (1991) Biochemistry, 30:10832; Clackson, T. et al. (1991) Nature, 352: 624; Marks, J. D. et al. (1991), J. Mol. Biol., 222:581; Kang, A.S. et al. (1991) Proc. Natl. Acad. Sci. USA, 88:8363) libraries on phage have been used for screening millions of polypeptides or oligopeptides for ones with specific binding properties (Smith, G. P. (1991) Current Opin. Biotechnol., 2:668). Sorting phage libraries of random mutants requires a strategy for constructing and propagating a large number of variants, a procedure for affinity purification using the target receptor, and a means of evaluating the results of binding enrichments. U.S. Patent Nos. 5,223,409, 5,403,484, 5,571,689, and 5,663,143.

Although most phage display methods have used filamentous phage, lambdoid phage display systems (WO 95/34683; U.S. 5,627,024), T4 phage display systems (Ren, Z-J. et al. (1998) Gene 215:439; Zhu, Z. (1997) CAN 33:534; Jiang, J. et al. (1997) can 128:44380; Ren, Z-J. et al. (1997) CAN 127:215644; Ren, Z-J. (1996) Protein Sci. 5:1833; Efimov, V. P. et al. (1995) Virus Genes 10:173) and T7 phage display systems (Smith, G. P. and Scott, J.K. (1993) Methods in Enzymology, 217, 228–257; U.S. 5,766,905) are also known.

Many other improvements and variations of the basic phage display concept have now been developed. These improvements enhance the ability of display systems to screen peptide libraries for binding to selected target molecules and to display functional proteins with the potential of screening these proteins for desired properties. Combinatorial reaction devices for phage display reactions have been developed (WO 98/14277) and phage display libraries have been used to analyze and control bimolecular interactions (WO 98/20169; WO 98/20159) and properties of constrained helical peptides (WO 98/20036). WO 97/35196 describes a method of isolating an affinity ligand in which a phage display library is contacted with one solution in which the ligand will bind to a target molecule and a second solution in which the affinity ligand will not bind to the target molecule, to selectively isolate binding ligands. WO 97/46251 describes a method of biopanning a random phage display library with an affinity purified antibody and then isolating binding phage, followed by a micropanning process using microplate wells to isolate high affinity binding phage. The use of Staphlylococcus aureus protein A as an affinity tag has also been reported (Li et al. (1998) Mol Biotech., 9:187). WO 97/47314 describes the use of substrate subtraction libraries to distinguish enzyme specificities using a combinatorial library which may be a phage display library. A method for selecting enzymes suitable for use in detergents using phage display is described in WO 97/09446. Additional methods of selecting specific binding proteins are described in U.S. Patent Nos. 5,498,538, 5,432,018, and WO 98/15833.

Methods of generating peptide libraries and screening these libraries are also disclosed in U.S. Patent Nos. 5,723,286, 5,432,018, 5,580,717, 5,427,908, 5,498,530, 5,770,434, 5,734,018, 5,698,426, 5,763,192, and 5,723,323.

C. TAT Binding Organic Molecules

TAT binding organic molecules are organic molecules other than oligopeptides or antibodies as defined herein that bind, preferably specifically, to a TAT polypeptide as described herein. TAT binding organic molecules may be identified and chemically synthesized using known methodology (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585). TAT binding organic molecules are usually less than about 2000 daltons in size, alternatively less than about 1500, 750, 500, 250 or 200 daltons in size, wherein such organic molecules

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To select for an anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule which induces cell death, loss of membrane integrity as indicated by, e.g., propidium iodide (PI), trypan blue or 7AAD uptake may be assessed relative to control. A PI uptake assay can be performed in the absence of complement and immune effector cells. TAT polypeptide-expressing tumor cells are incubated with medium alone or medium containing the appropriate anti-TAT antibody (e.g., at about 10 µg/ml), TAT binding oligopeptide or TAT binding organic molecule. The cells are incubated for a 3 day time period. Following each treatment, cells are washed and aliquoted into 35 mm strainer-capped 12 x 75 tubes (1ml per tube, 3 tubes per treatment group) for removal of cell clumps. Tubes then receive PI (10 µg/ml). Samples may be analyzed using a FACSCAN® flow cytometer and FACSCONVERT® CellQuest software (Becton Dickinson). Those anti-TAT antibodies, TAT binding oligopeptides or TAT binding organic molecules that induce statistically significant levels of cell death as determined by PI uptake may be selected as cell death-inducing anti-TAT antibodies, TAT binding oligopeptides or TAT binding organic molecules.

To screen for antibodies, oligopeptides or other organic molecules which bind to an epitope on a TAT polypeptide bound by an antibody of interest, a routine cross-blocking assay such as that described in Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory, Ed Harlow and David Lane (1988), can be performed. This assay can be used to determine if a test antibody, oligopeptide or other organic molecule binds the same site or epitope as a known anti-TAT antibody. Alternatively, or additionally, epitope mapping can be performed by methods known in the art. For example, the antibody sequence can be mutagenized such as by alanine scanning, to identify contact residues. The mutant antibody is initially tested for binding with polyclonal antibody to ensure proper folding. In a different method, peptides corresponding to different regions of a TAT polypeptide can be used in competition assays with the test antibodies or with a test antibody and an antibody with a characterized or known epitope.

E. Antibody Dependent Enzyme Mediated Prodrug Therapy (ADEPT)

The antibodies of the present invention may also be used in ADEPT by conjugating the antibody to a prodrug-activating enzyme which converts a prodrug (e.g., a peptidyl chemotherapeutic agent, see WO81/01145) to an active anti-cancer drug. See, for example, WO 88/07378 and U.S. Patent No. 4,975,278.

The enzyme component of the immunoconjugate useful for ADEPT includes any enzyme capable of acting on a prodrug in such a way so as to covert it into its more active, cytotoxic form.

Enzymes that are useful in the method of this invention include, but are not limited to, alkaline phosphatase useful for converting phosphate-containing prodrugs into free drugs; arylsulfatase useful for converting sulfate-containing prodrugs into free drugs; cytosine deaminase useful for converting non-toxic 5-fluorocytosine into the anti-cancer drug, 5-fluorouracil; proteases, such as serratia protease, thermolysin, subtilisin, carboxypeptidases and cathepsins (such as cathepsins B and L), that are useful for converting peptide-containing prodrugs into free drugs; D-alanylcarboxypeptidases, useful for converting prodrugs that contain D-amino acid substituents; carbohydrate-cleaving enzymes such as β-galactosidase and neuraminidase useful for converting glycosylated prodrugs into free drugs; β-lactamase useful for converting drugs derivatized with β-lactams into free drugs; and penicillin amidases, such as penicillin V amidase or penicillin G amidase, useful

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for converting drugs derivatized at their amine nitrogens with phenoxyacetyl or phenylacetyl groups, respectively, into free drugs. Alternatively, antibodies with enzymatic activity, also known in the art as "abzymes", can be used to convert the prodrugs of the invention into free active drugs (see, e.g., Massey, Nature 328:457-458 (1987)). Antibody-abzyme conjugates can be prepared as described herein for delivery of the abzyme to a tumor cell population.

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The enzymes of this invention can be covalently bound to the anti-TAT antibodies by techniques well known in the art such as the use of the heterobifunctional crosslinking reagents discussed above. Alternatively, fusion proteins comprising at least the antigen binding region of an antibody of the invention linked to at least a functionally active portion of an enzyme of the invention can be constructed using recombinant DNA techniques well known in the art (see, e.g., Neuberger et al., Nature 312:604-608 (1984).

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F. Full-Length TAT Polypeptides

The present invention also provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as TAT polypeptides. In particular, cDNAs (partial and full-length) encoding various TAT polypeptides have been identified and isolated, as disclosed in further detail in the Examples below.

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As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the TAT polypeptides and encoding nucleic acids described herein, in some cases, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

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G. Anti-TAT Antibody and TAT Polypeptide Variants

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In addition to the anti-TAT antibodies and full-length native sequence TAT polypeptides described herein, it is contemplated that anti-TAT antibody and TAT polypeptide variants can be prepared. Anti-TAT antibody and TAT polypeptide variants can be prepared by introducing appropriate nucleotide changes into the encoding DNA, and/or by synthesis of the desired antibody or polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the anti-TAT antibody or TAT polypeptide, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

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Variations in the anti-TAT antibodies and TAT polypeptides described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the antibody or polypeptide that results in a change in the amino acid sequence as compared with the native sequence antibody or polypeptide. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the anti-TAT antibody or TAT polypeptide. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the anti-TAT antibody or

TAT polypeptide with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

Anti-TAT antibody and TAT polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native antibody or protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the anti-TAT antibody or TAT polypeptide.

Anti-TAT antibody and TAT polypeptide fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating antibody or polypeptide fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired antibody or polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, anti-TAT antibody and TAT polypeptide fragments share at least one biological and/or immunological activity with the native anti-TAT antibody or TAT polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

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Table 6

	Original	Exemplary	Preferred
	Residue	Substitutions	Substitutions
	Ala (A)	val; leu; ile	val
5	Arg (R)	lys; gln; asn	lys
	Asn (N)	gln; his; lys; arg	gln
	Asp (D)	glu	glu
	Cys (C)	ser	ser
	Gln (Q)	asn	asn
10	Glu (E)	asp	asp
	Gly (G)	pro; ala	ala
	His (H)	asn; gln; lys; arg	arg
	Ile (I)	leu; val; met; ala; phe;	C
15		norleucine	leu
	Leu (L)	norleucine; ile; val;	
		met; ala; phe	ile
	Lys (K)	arg; gln; asn	arg
	Met (M)	leu; phe; ile	leu
	Phe (F)	leu; val; ile; ala; tyr	leu
25	Pro (P)	ala	ala
	Ser (S)	thr	thr
	Thr (T)	ser	ser
	Trp (W)	tyr; phe	tyr
	Tyr (Y)	trp; phe; thr; ser	phe
	Val (V)	ile; leu; met; phe;	•
		ala; norleucine	leu

Substantial modifications in function or immunological identity of the anti-TAT antibody or TAT polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- (1) hydrophobic: norleucine, met, ala, val, leu, ile;
- (2) neutral hydrophilic: cys, ser, thr;
- 35 (3) acidic: asp, glu;

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- (4) basic: asn, gln, his, lys, arg;
- (5) residues that influence chain orientation: gly, pro; and
- (6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al. Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al., Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the anti-TAT antibody or TAT polypeptide variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244:1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

Any cysteine residue not involved in maintaining the proper conformation of the anti-TAT antibody or TAT polypeptide also may be substituted, generally with serine, to improve the oxidative stability of the molecule and prevent aberrant crosslinking. Conversely, cysteine bond(s) may be added to the anti-TAT antibody or TAT polypeptide to improve its stability (particularly where the antibody is an antibody fragment such as an Fv fragment).

A particularly preferred type of substitutional variant involves substituting one or more hypervariable region residues of a parent antibody (e.g., a humanized or human antibody). Generally, the resulting variant(s) selected for further development will have improved biological properties relative to the parent antibody from which they are generated. A convenient way for generating such substitutional variants involves affinity maturation using phage display. Briefly, several hypervariable region sites (e.g., 6-7 sites) are mutated to generate all possible amino substitutions at each site. The antibody variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (e.g., binding affinity) as herein disclosed. In order to identify candidate hypervariable region sites for modification, alanine scanning mutagenesis can be performed to identify hypervariable region residues contributing significantly to antigen binding. Alternatively, or additionally, it may be beneficial to analyze a crystal structure of the antigen-antibody complex to identify contact points between the antibody and human TAT polypeptide. Such contact residues and neighboring residues are candidates for substitution according to the techniques elaborated herein. Once such variants are generated, the panel of variants is subjected to screening as described herein and antibodies with superior properties in one or more relevant assays may be selected for further development.

Nucleic acid molecules encoding amino acid sequence variants of the anti-TAT antibody are prepared by a variety of methods known in the art. These methods include, but are not limited to, isolation from a natural source (in the case of naturally occurring amino acid sequence variants) or preparation by oligonucleotide-

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mediated (or site-directed) mutagenesis, PCR mutagenesis, and cassette mutagenesis of an earlier prepared variant or a non-variant version of the anti-TAT antibody.

H. Modifications of Anti-TAT Antibodies and TAT Polypeptides

Covalent modifications of anti-TAT antibodies and TAT polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of an anti-TAT antibody or TAT polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the anti-TAT antibody or TAT polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking anti-TAT antibody or TAT polypeptide to a water-insoluble support matrix or surface for use in the method for purifying anti-TAT antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, <u>Proteins: Structure and Molecular Properties</u>, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the anti-TAT antibody or TAT polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the antibody or polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence anti-TAT antibody or TAT polypeptide (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence anti-TAT antibody or TAT polypeptide. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Glycosylation of antibodies and other polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tripeptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tripeptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-aceylgalactosamine, galactose, or xylose to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

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Addition of glycosylation sites to the anti-TAT antibody or TAT polypeptide is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tripeptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the sequence of the original anti-TAT antibody or TAT polypeptide (for O-linked glycosylation sites). The anti-TAT antibody or TAT polypeptide amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the anti-TAT antibody or TAT polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the anti-TAT antibody or TAT polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, <u>CRC Crit. Rev. Biochem.</u>, pp. 259-306 (1981).

Removal of carbohydrate moieties present on the anti-TAT antibody or TAT polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., <u>Arch. Biochem. Biophys.</u>, <u>259</u>:52 (1987) and by Edge et al., <u>Anal. Biochem.</u>, <u>118</u>:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., <u>Meth. Enzymol.</u>, 138:350 (1987).

Another type of covalent modification of anti-TAT antibody or TAT polypeptide comprises linking the antibody or polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. The antibody or polypeptide also may be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization (for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate) microcapsules, respectively), in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nanoparticles and nanocapsules), or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, 16th edition, Oslo, A., Ed., (1980).

The anti-TAT antibody or TAT polypeptide of the present invention may also be modified in a way to form chimeric molecules comprising an anti-TAT antibody or TAT polypeptide fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the anti-TAT antibody or TAT polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the anti-TAT antibody or TAT polypeptide. The presence of such epitope-tagged forms of the anti-TAT antibody or TAT polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the anti-TAT

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antibody or TAT polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an α-tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

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In an alternative embodiment, the chimeric molecule may comprise a fusion of the anti-TAT antibody or TAT polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of an anti-TAT antibody or TAT polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH₂ and CH₃, or the hinge, CH₁, CH₂ and CH₃ regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27, 1995.

I. Preparation of Anti-TAT Antibodies and TAT Polypeptides

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The description below relates primarily to production of anti-TAT antibodies and TAT polypeptides by culturing cells transformed or transfected with a vector containing anti-TAT antibody- and TAT polypeptide-encoding nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare anti-TAT antibodies and TAT polypeptides. For instance, the appropriate amino acid sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. In vitro protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the anti-TAT antibody or TAT polypeptide may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the desired anti-TAT antibody or TAT polypeptide.

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1. Isolation of DNA Encoding Anti-TAT Antibody or TAT Polypeptide

DNA encoding anti-TAT antibody or TAT polypeptide may be obtained from a cDNA library prepared from tissue believed to possess the anti-TAT antibody or TAT polypeptide mRNA and to express it at a detectable level. Accordingly, human anti-TAT antibody or TAT polypeptide DNA can be conveniently obtained from a cDNA library prepared from human tissue. The anti-TAT antibody- or TAT polypeptide-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated

nucleic acid synthesis).

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Libraries can be screened with probes (such as oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding anti-TAT antibody or TAT polypeptide is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

Techniques for screening a cDNA library are well known in the art. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ³²P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., <u>supra</u>, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. <u>Selection and Transformation of Host Cells</u>

Host cells are transfected or transformed with expression or cloning vectors described herein for anti-TAT antibody or TAT polypeptide production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in <u>Mammalian Cell Biotechnology</u>: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., <u>supra.</u>.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl₂, CaPO₄, liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., <u>supra</u>, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., <u>Gene</u>, <u>23</u>:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, <u>Virology</u>,

52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., <u>J. Bact.</u>, <u>130</u>:946 (1977) and Hsiao et al., <u>Proc. Natl. Acad. Sci. (USA)</u>, <u>76</u>:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., <u>Methods in Enzymology</u>, 185:527-537 (1990) and Mansour et al., <u>Nature</u>, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as E. coli. Various E. coli strains are publicly available, such as E. coli K12 strain MM294 (ATCC 31,446); E. coli X1776 (ATCC 31,537); E. coli strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as Escherichia, e.g., E. coli, Enterobacter, Erwinia, Klebsiella, Proteus, Salmonella, e.g., Salmonella typhimurium, Serratia, e.g., Serratia marcescans, and Shigella, as well as Bacilli such as B. subtilis and B. licheniformis (e.g., B. licheniformis 41P disclosed in DD 266,710 published 12 April 1989), Pseudomonas such as P. aeruginosa, and Streptomyces. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including E. coli W3110 strain 1A2, which has the complete genotype tonA; E. coli W3110 strain 9E4, which has the complete genotype tonA ptr3; E. coli W3110 strain 27C7 (ATCC 55,244), which has the complete genotype tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan'; E. coli W3110 strain 37D6, which has the complete genotype tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG karl; E. coli W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant degP deletion mutation; and an E. coli strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, in vitro methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

Full length antibody, antibody fragments, and antibody fusion proteins can be produced in bacteria, in particular when glycosylation and Fc effector function are not needed, such as when the therapeutic antibody is conjugated to a cytotoxic agent (e.g., a toxin) and the immunoconjugate by itself shows effectiveness in tumor cell destruction. Full length antibodies have greater half life in circulation. Production in E. coli is faster and more cost efficient. For expression of antibody fragments and polypeptides in bacteria, see, e.g., U.S. 5,648,237 (Carter et. al.), U.S. 5,789,199 (Joly et al.), and U.S. 5,840,523 (Simmons et al.) which describes translation initiation regio (TIR) and signal sequences for optimizing expression and secretion, these patents incorporated herein by reference. After expression, the antibody is isolated from the E. coli cell paste in a soluble fraction and can be purified through, e.g., a protein A or G column depending on the isotype. Final purification can be carried out similar to the process for purifying antibody expressed e.g., in CHO cells.

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In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for anti-TAT antibody- or TAT polypeptide-encoding vectors. Saccharomyces cerevisiae is a commonly used lower eukaryotic host microorganism. Others include Schizosaccharomyces pombe (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); Kluyveromyces hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., K. lactis (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), K. fragilis (ATCC 12,424), K. bulgaricus (ATCC 16,045), K. wickeramii (ATCC 24,178), K. waltii (ATCC 56,500), K. drosophilarum (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), K. thermotolerans, and K. marxianus; yarrowia (EP 402,226); Pichia pastoris (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); Candida; Trichoderma reesia (EP 244,234); Neurospora crassa (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); Schwanniomyces such as Schwanniomyces occidentalis (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., Neurospora, Penicillium, Tolypocladium (WO 91/00357 published 10 January 1991), and Aspergillus hosts such as A. nidulans (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and A. niger (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylotropic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of Hansenula, Candida, Kloeckera, Pichia, Saccharomyces, Torulopsis, and Rhodotorula. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylotrophs, 269 (1982).

Suitable host cells for the expression of glycosylated anti-TAT antibody or TAT polypeptide are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as Drosophila S2 and Spodoptera Sf9, as well as plant cells, such as cell cultures of cotton, corn, potato, soybean, petunia, tomato, and tobacco. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as Spodoptera frugiperda (caterpillar), Aedes aegypti (mosquito), Aedes albopictus (mosquito), Drosophila melanogaster (fruitfly), and Bombyx mori have been identified. A variety of viral strains for transfection are publicly available, e.g., the L-1 variant of Autographa californica NPV and the Bm-5 strain of Bombyx mori NPV, and such viruses may be used as the virus herein according to the present invention, particularly for transfection of Spodoptera frugiperda cells.

However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (tissue culture) has become a routine procedure. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol. 36:59 (1977)); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO, Urlaub et al., Proc. Natl. Acad. Sci. USA77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod. 23:243-251 (1980)); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2,

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HB 8065); mouse mammary tumor (MMT 060562, ATCC CCL51); TRI cells (Mather et al., Annals N.Y. Acad. Sci. 383:44-68 (1982)); MRC 5 cells; FS4 cells; and a human hepatoma line (Hep G2).

Host cells are transformed with the above-described expression or cloning vectors for anti-TAT antibody or TAT polypeptide production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

3. Selection and Use of a Replicable Vector

The nucleic acid (e.g., cDNA or genomic DNA) encoding anti-TAT antibody or TAT polypeptide may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

The TAT may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the anti-TAT antibody- or TAT polypeptide-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including Saccharomyces and Kluyveromyces α -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the C. albicans glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification

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of cells competent to take up the anti-TAT antibody- or TAT polypeptide-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., <u>Proc. Natl. Acad. Sci. USA</u>, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., <u>Nature</u>, 282:39 (1979); Kingsman et al., <u>Gene</u>, 7:141 (1979); Tschemper et al., <u>Gene</u>, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, <u>Genetics</u>, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the anti-TAT antibodyor TAT polypeptide-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a
variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include theplactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544
(1979)], alkaline phosphatase, a tryptophan (trp) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980);
EP 36,776], and hybrid promoters such as the tac promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:2125 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably
linked to the DNA encoding anti-TAT antibody or TAT polypeptide.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

Anti-TAT antibody or TAT polypeptide transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the anti-TAT antibody or TAT polypeptide by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the

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late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the anti-TAT antibody or TAT polypeptide coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding anti-TAT antibody or TAT polypeptide.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of anti-TAT antibody or TAT polypeptide in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Culturing the Host Cells

The host cells used to produce the anti-TAT antibody or TAT polypeptide of this invention may be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium ((MEM), (Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium ((DMEM), Sigma) are suitable for culturing the host cells. In addition, any of the media described in Ham et allMeth. Enz. 58:44 (1979), Barnes et al., Anal. Biochem.102:255 (1980), U.S. Pat. Nos. 4,767,704; 4,657,866; 4,927,762; 4,560,655; or 5,122,469; WO 90/03430; WO 87/00195; or U.S. Patent Re. 30,985 may be used as culture media for the host cells. Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleotides (such as adenosine and thymidine), antibiotics (such as GENTAMYCINTM drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art. The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

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5. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or in situ hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence TAT polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to TAT DNA and encoding a specific antibody epitope.

6. Purification of Anti-TAT Antibody and TAT Polypeptide

Forms of anti-TAT antibody and TAT polypeptide may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of anti-TAT antibody and TAT polypeptide can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify anti-TAT antibody and TAT polypeptide from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the anti-TAT antibody and TAT polypeptide. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular anti-TAT antibody or TAT polypeptide produced.

When using recombinant techniques, the antibody can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the antibody is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, are removed, for example, by centrifugation or ultrafiltration. Carter et al., <u>Bio/Technology</u> 10:163-167 (1992) describe a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli*. Briefly, cell paste is thawed in the presence of sodium

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acetate (pH 3.5), EDTA, and phenylmethylsulfonylfluoride (PMSF) over about 30 min. Cell debris can be removed by centrifugation. Where the antibody is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis and antibiotics may be included to prevent the growth of adventitious contaminants.

The antibody composition prepared from the cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being the preferred purification technique. The suitability of protein A as an affinity ligand depends on the species and isotype of any immunoglobulin Fc domain that is present in the antibody. Protein A can be used to purify antibodies that are based on human $\gamma 1$, $\gamma 2$ or $\gamma 4$ heavy chains (Lindmark et al., J. Immunol. Meth. 62:1-13 (1983)). Protein G is recommended for all mouse isotypes and for human y3 (Guss et al., EMBO J. 5:15671575 (1986)). The matrix to which the affinity ligand is attached is most often agarose, but other Mechanically stable matrices such as controlled pore glass or matrices are available. poly(styrenedivinyl)benzene allow for faster flow rates and shorter processing times than can be achieved with agarose. Where the antibody comprises a C₁3 domain, the Bakerbond ABXTesin (J. T. Baker, Phillipsburg, NJ) is useful for purification. Other techniques for protein purification such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on heparin SEPHAROSE™ chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), chromatofocusing, SDS-PAGE, and ammonium sulfate precipitation are also available depending on the antibody to be recovered.

Following any preliminary purification step(s), the mixture comprising the antibody of interest and contaminants may be subjected to low pH hydrophobic interaction chromatography using an elution buffer at a pH between about 2.5-4.5, preferably performed at low salt concentrations (e.g., from about 0-0.25M salt).

J. <u>Pharmaceutical Formulations</u>

Therapeutic formulations of the anti-TAT antibodies, TAT binding oligopeptides, TAT binding organic molecules and/or TAT polypeptides used in accordance with the present invention are prepared for storage by mixing the antibody, polypeptide, oligopeptide or organic molecule having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as acetate, Tris, phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine,

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histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; tonicifiers such as trehalose and sodium chloride; sugars such as sucrose, mannitol, trehalose or sorbitol; surfactant such as polysorbate; salt-forming counter-ions such as sodium; metal complexes (e.g., Zn-protein complexes); and/or non-ionic surfactants such as TWEEN®, PLURONICS® or polyethylene glycol (PEG). The antibody preferably comprises the antibody at a concentration of between 5-200 mg/ml, preferably between 10-100 mg/ml.

The formulations herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. For example, in addition to an anti-TAT antibody, TAT binding oligopeptide, or TAT binding organic molecule, it may be desirable to include in the one formulation, an additional antibody, e.g., a second anti-TAT antibody which binds a different epitope on the TAT polypeptide, or an antibody to some other target such as a growth factor that affects the growth of the particular cancer. Alternatively, or additionally, the composition may further comprise a chemotherapeutic agent, cytotoxic agent, cytokine, growth inhibitory agent, anti-hormonal agent, and/or cardioprotectant. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in <u>Remington's Pharmaceutical Sciences</u>, 16th edition, Osol, A. Ed. (1980).

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semi-permeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylenevinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT® (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

K. <u>Diagnosis and Treatment with Anti-TAT Antibodies, TAT Binding Oligopeptides and TAT</u>

Binding Organic Molecules

To determine TAT expression in the cancer, various diagnostic assays are available. In one embodiment, TAT polypeptide overexpression may be analyzed by immunohistochemistry (IHC). Parrafin embedded tissue sections from a tumor biopsy may be subjected to the IHC assay and accorded a TAT protein staining intensity criteria as follows:

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Score 0 - no staining is observed or membrane staining is observed in less than 10% of tumor cells.

Score 1+ - a faint/barely perceptible membrane staining is detected in more than 10% of the tumor cells. The cells are only stained in part of their membrane.

Score 2+ - a weak to moderate complete membrane staining is observed in more than 10% of the tumor cells.

Score 3+ - a moderate to strong complete membrane staining is observed in more than 10% of the tumor cells.

Those tumors with 0 or 1+ scores for TAT polypeptide expression may be characterized as not overexpressing TAT, whereas those tumors with 2+ or 3+ scores may be characterized as overexpressing TAT.

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Alternatively, or additionally, FISH assays such as the INFORM® (sold by Ventana, Arizona) or PATHVISION® (Vysis, Illinois) may be carried out on formalin-fixed, paraffin-embedded tumor tissue to determine the extent (if any) of TAT overexpression in the tumor.

TAT overexpression or amplification may be evaluated using an *in vivo* diagnostic assay, e.g., by administering a molecule (such as an antibody, oligopeptide or organic molecule) which binds the molecule to be detected and is tagged with a detectable label (e.g., a radioactive isotope or a fluorescent label) and externally scanning the patient for localization of the label.

As described above, the anti-TAT antibodies, oligopeptides and organic molecules of the invention have various non-therapeutic applications. The anti-TAT antibodies, oligopeptides and organic molecules of the present invention can be useful for diagnosis and staging of TAT polypeptide-expressing cancers (e.g., in radioimaging). The antibodies, oligopeptides and organic molecules are also useful for purification or immunoprecipitation of TAT polypeptide from cells, for detection and quantitation of TAT polypeptide in vitro, e.g., in an ELISA or a Western blot, to kill and eliminate TAT-expressing cells from a population of mixed cells as a step in the purification of other cells.

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Currently, depending on the stage of the cancer, cancer treatment involves one or a combination of the following therapies: surgery to remove the cancerous tissue, radiation therapy, and chemotherapy. Anti-TAT antibody, oligopeptide or organic molecule therapy may be especially desirable in elderly patients who do not tolerate the toxicity and side effects of chemotherapy well and in metastatic disease where radiation therapy has limited usefulness. The tumor targeting anti-TAT antibodies, oligopeptides and organic molecules of the invention are useful to alleviate TAT-expressing cancers upon initial diagnosis of the disease or during relapse. For therapeutic applications, the anti-TAT antibody, oligopeptide or organic molecule can be used alone, or in combination therapy with, e.g., hormones, antiangiogens, or radiolabelled compounds, or with surgery, cryotherapy, and/or radiotherapy. Anti-TAT antibody, oligopeptide or organic molecule treatment can be administered in conjunction with other forms of conventional therapy, either consecutively with, pre- or post-conventional therapy. Chemotherapeutic drugs such as TAXOTERE® (docetaxel), TAXOL® (palictaxel), estramustine and mitoxantrone are used in treating cancer, in particular, in good risk patients. In the present method of the invention for treating or alleviating cancer, the cancer patient can be administered anti-TAT

antibody, oligopeptide or organic molecule in conjuction with treatment with the one or more of the preceding chemotherapeutic agents. In particular, combination therapy with palictaxel and modified derivatives (see, e.g., EP0600517) is contemplated. The anti-TAT antibody, oligopeptide or organic molecule will be administered with a therapeutically effective dose of the chemotherapeutic agent. In another embodiment, the anti-TAT antibody, oligopeptide or organic molecule is administered in conjunction with chemotherapy to enhance the activity and efficacy of the chemotherapeutic agent, e.g., paclitaxel. The Physicians' Desk Reference (PDR) discloses dosages of these agents that have been used in treatment of various cancers. The dosing regimen and dosages of these aforementioned chemotherapeutic drugs that are therapeutically effective will depend on the particular cancer being treated, the extent of the disease and other factors familiar to the physician of skill in the art and can be determined by the physician.

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In one particular embodiment, a conjugate comprising an anti-TAT antibody, oligopeptide or organic molecule conjugated with a cytotoxic agent is administered to the patient. Preferably, the immunoconjugate bound to the TAT protein is internalized by the cell, resulting in increased therapeutic efficacy of the immunoconjugate in killing the cancer cell to which it binds. In a preferred embodiment, the cytotoxic agent targets or interferes with the nucleic acid in the cancer cell. Examples of such cytotoxic agents are described above and include maytansinoids, calicheamicins, ribonucleases and DNA endonucleases.

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The anti-TAT antibodies, oligopeptides, organic molecules or toxin conjugates thereof are administered to a human patient, in accord with known methods, such as intravenous administration, e.g.,, as a bolus or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intracerobrospinal, subcutaneous, intra-articular, intrasynovial, intrathecal, oral, topical, or inhalation routes. Intravenous or subcutaneous administration of the antibody, oligopeptide or organic molecule is preferred.

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Other therapeutic regimens may be combined with the administration of the anti-TAT antibody, oligopeptide or organic molecule. The combined administration includes co-administration, using separate formulations or a single pharmaceutical formulation, and consecutive administration in either order, wherein preferably there is a time period while both (or all) active agents simultaneously exert their biological activities. Preferably such combined therapy results in a synergistic therapeutic effect.

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It may also be desirable to combine administration of the anti-TAT antibody or antibodies, oligopeptides or organic molecules, with administration of an antibody directed against another tumor antigen associated with the particular cancer.

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In another embodiment, the therapeutic treatment methods of the present invention involves the combined administration of an anti-TAT antibody (or antibodies), oligopeptides or organic molecules and one or more chemotherapeutic agents or growth inhibitory agents, including co-administration of cocktails of different chemotherapeutic agents. Chemotherapeutic agents include estramustine phosphate, prednimustine, cisplatin, 5-fluorouracil, melphalan, cyclophosphamide, hydroxyurea and hydroxyureataxanes (such as paclitaxel and doxetaxel) and/or anthracycline antibiotics. Preparation and dosing schedules for such chemotherapeutic agents may be used according to manufacturers' instructions or as determined empirically by the skilled practitioner. Preparation and dosing schedules for such chemotherapy are also described in Chemotherapy

Service Ed., M.C. Perry, Williams & Wilkins, Baltimore, MD (1992).

The antibody, oligopeptide or organic molecule may be combined with an anti-hormonal compound; e.g., an anti-estrogen compound such as tamoxifen; an anti-progesterone such as onapristone (see, EP 616 812); or an anti-androgen such as flutamide, in dosages known for such molecules. Where the cancer to be treated is androgen independent cancer, the patient may previously have been subjected to anti-androgen therapy and, after the cancer becomes androgen independent, the anti-TAT antibody, oligopeptide or organic molecule (and optionally other agents as described herein) may be administered to the patient.

Sometimes, it may be beneficial to also co-administer a cardioprotectant (to prevent or reduce myocardial dysfunction associated with the therapy) or one or more cytokines to the patient. In addition to the above therapeutic regimes, the patient may be subjected to surgical removal of cancer cells and/or radiation therapy, before, simultaneously with, or post antibody, oligopeptide or organic molecule therapy. Suitable dosages for any of the above co-administered agents are those presently used and may be lowered due to the combined action (synergy) of the agent and anti-TAT antibody, oligopeptide or organic molecule.

For the prevention or treatment of disease, the dosage and mode of administration will be chosen by the physician according to known criteria. The appropriate dosage of antibody, oligopeptide or organic molecule will depend on the type of disease to be treated, as defined above, the severity and course of the disease, whether the antibody, oligopeptide or organic molecule is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the antibody, oligopeptide or organic molecule, and the discretion of the attending physician. The antibody, oligopeptide or organic molecule is suitably administered to the patient at one time or over a series of treatments. Preferably, the antibody, oligopeptide or organic molecule is administered by intravenous infusion or by subcutaneous injections. Depending on the type and severity of the disease, about 1 µg/kg to about 50 mg/kg body weight (e.g., about 0.1-15mg/kg/dose) of antibody can be an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. A dosing regimen can comprise administering an initial loading dose of about 4 mg/kg, followed by a weekly maintenance dose of about 2 mg/kg of the anti-TAT antibody. However, other dosage regimens may be useful. A typical daily dosage might range from about 1 µg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment is sustained until a desired suppression of disease symptoms occurs. The progress of this therapy can be readily monitored by conventional methods and assays and based on criteria known to the physician or other persons of skill in the art.

Aside from administration of the antibody protein to the patient, the present application contemplates administration of the antibody by gene therapy. Such administration of nucleic acid encoding the antibody is encompassed by the expression "administering a therapeutically effective amount of an antibody". See, for example, WO96/07321 published March 14, 1996 concerning the use of gene therapy to generate intracellular antibodies.

There are two major approaches to getting the nucleic acid (optionally contained in a vector) into the patient's cells; in vivo and ex vivo. For in vivo delivery the nucleic acid is injected directly into the patient,

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usually at the site where the antibody is required. For ex vivo treatment, the patient's cells are removed, the nucleic acid is introduced into these isolated cells and the modified cells are administered to the patient either directly or, for example, encapsulated within porous membranes which are implanted into the patient (see, e.g., U.S. Patent Nos. 4,892,538 and 5,283,187). There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells in vitro, or in vivo in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells in vitro include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. A commonly used vector for ex vivo delivery of the gene is a retroviral vector.

The currently preferred *in vivo* nucleic acid transfer techniques include transfection with viral vectors (such as adenovirus, Herpes simplex I virus, or adeno-associated virus) and lipid-based systems (useful lipids for lipid-mediated transfer of the gene are DOTMA, DOPE and DC-Chol, for example). For review of the currently known gene marking and gene therapy protocols see Anderson et al., <u>Science</u> 256:808-813 (1992). See also WO 93/25673 and the references cited therein.

The anti-TAT antibodies of the invention can be in the different forms encompassed by the definition of "antibody" herein. Thus, the antibodies include full length or intact antibody, antibody fragments, native sequence antibody or amino acid variants, humanized, chimeric or fusion antibodies, immunoconjugates, and functional fragments thereof. In fusion antibodies an antibody sequence is fused to a heterologous polypeptide sequence. The antibodies can be modified in the Fc region to provide desired effector functions. As discussed in more detail in the sections herein, with the appropriate Fc regions, the naked antibody bound on the cell surface can induce cytotoxicity, e.g., via antibody-dependent cellular cytotoxicity (ADCC) or by recruiting complement in complement dependent cytotoxicity, or some other mechanism. Alternatively, where it is desirable to eliminate or reduce effector function, so as to minimize side effects or therapeutic complications, certain other Fc regions may be used.

In one embodiment, the antibody competes for binding or bind substantially to, the same epitope as the antibodies of the invention. Antibodies having the biological characteristics of the present anti-TAT antibodies of the invention are also contemplated, specifically including the *in vivo* tumor targeting and any cell proliferation inhibition or cytotoxic characteristics.

Methods of producing the above antibodies are described in detail herein.

The present anti-TAT antibodies, oligopeptides and organic molecules are useful for treating a TAT-expressing cancer or alleviating one or more symptoms of the cancer in a mammal. Such a cancer includes prostate cancer, cancer of the urinary tract, lung cancer, breast cancer, colon cancer and ovarian cancer, more specifically, prostate adenocarcinoma, renal cell carcinomas, colorectal adenocarcinomas, lung adenocarcinomas, lung squamous cell carcinomas, and pleural mesothelioma. The cancers encompass metastatic cancers of any of the preceding. The antibody, oligopeptide or organic molecule is able to bind to at least a portion of the cancer cells that express TAT polypeptide in the mammal. In a preferred embodiment, the antibody, oligopeptide or organic molecule is effective to destroy or kill TAT-expressing tumor cells or inhibit

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the growth of such tumor cells, in vitro or in vivo, upon binding to TAT polypeptide on the cell. Such an antibody includes a naked anti-TAT antibody (not conjugated to any agent). Naked antibodies that have cytotoxic or cell growth inhibition properties can be further harnessed with a cytotoxic agent to render them even more potent in tumor cell destruction. Cytotoxic properties can be conferred to an anti-TAT antibody by, e.g., conjugating the antibody with a cytotoxic agent, to form an immunoconjugate as described herein. The cytotoxic agent or a growth inhibitory agent is preferably a small molecule. Toxins such as calicheamicin or a maytansinoid and analogs or derivatives thereof, are preferable.

The invention provides a composition comprising an anti-TAT antibody, oligopeptide or organic molecule of the invention, and a carrier. For the purposes of treating cancer, compositions can be administered to the patient in need of such treatment, wherein the composition can comprise one or more anti-TAT antibodies present as an immunoconjugate or as the naked antibody. In a further embodiment, the compositions can comprise these antibodies, oligopeptides or organic molecules in combination with other therapeutic agents such as cytotoxic or growth inhibitory agents, including chemotherapeutic agents. The invention also provides formulations comprising an anti-TAT antibody, oligopeptide or organic molecule of the invention, and a carrier. In one embodiment, the formulation is a therapeutic formulation comprising a pharmaceutically acceptable carrier.

Another aspect of the invention is isolated nucleic acids encoding the anti-TAT antibodies. Nucleic acids encoding both the H and L chains and especially the hypervariable region residues, chains which encode the native sequence antibody as well as variants, modifications and humanized versions of the antibody, are encompassed.

The invention also provides methods useful for treating a TAT polypeptide-expressing cancer or alleviating one or more symptoms of the cancer in a mammal, comprising administering a therapeutically effective amount of an anti-TAT antibody, oligopeptide or organic molecule to the mammal. The antibody, oligopeptide or organic molecule therapeutic compositions can be administered short term (acute) or chronic, or intermittent as directed by physician. Also provided are methods of inhibiting the growth of, and killing a TAT polypeptide-expressing cell.

The invention also provides kits and articles of manufacture comprising at least one anti-TAT antibody, oligopeptide or organic molecule. Kits containing anti-TAT antibodies, oligopeptides or organic molecules find use, e.g., for TAT cell killing assays, for purification or immunoprecipitation of TAT polypeptide from cells. For example, for isolation and purification of TAT, the kit can contain an anti-TAT antibody, oligopeptide or organic molecule coupled to beads (e.g., sepharose beads). Kits can be provided which contain the antibodies, oligopeptides or organic molecules for detection and quantitation of TAT *in vitro*, e.g., in an ELISA or a Western blot. Such antibody, oligopeptide or organic molecule useful for detection may be provided with a label such as a fluorescent or radiolabel.

L. Articles of Manufacture and Kits

Another embodiment of the invention is an article of manufacture containing materials useful for the treatment of anti-TAT expressing cancer. The article of manufacture comprises a container and a label or

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package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, etc. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition which is effective for treating the cancer condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). At least one active agent in the composition is an anti-TAT antibody, oligopeptide or organic molecule of the invention. The label or package insert indicates that the composition is used for treating cancer. The label or package insert will further comprise instructions for administering the antibody, oligopeptide or organic molecule composition to the cancer patient. Additionally, the article of manufacture may further comprise a second container comprising a pharmaceutically-acceptable buffer, such as bacteriostatic water for injection (BWFI), phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, and syringes.

Kits are also provided that are useful for various purposes, e.g., for TAT-expressing cell killing assays, for purification or immunoprecipitation of TAT polypeptide from cells. For isolation and purification of TAT polypeptide, the kit can contain an anti-TAT antibody, oligopeptide or organic molecule coupled to beads (e.g., sepharose beads). Kits can be provided which contain the antibodies, oligopeptides or organic molecules for detection and quantitation of TAT polypeptide in vitro, e.g., in an ELISA or a Western blot. As with the article of manufacture, the kit comprises a container and a label or package insert on or associated with the container. The container holds a composition comprising at least one anti-TAT antibody, oligopeptide or organic molecule of the invention. Additional containers may be included that contain, e.g., diluents and buffers, control antibodies. The label or package insert may provide a description of the composition as well as instructions for the intended in vitro or diagnostic use.

M. Uses for TAT Polypeptides and TAT-Polypeptide Encoding Nucleic Acids

Nucleotide sequences (or their complement) encoding TAT polypeptides have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA probes. TAT-encoding nucleic acid will also be useful for the preparation of TAT polypeptides by the recombinant techniques described herein, wherein those TAT polypeptides may find use, for example, in the preparation of anti-TAT antibodies as described herein.

The full-length native sequence TAT gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length TAT cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of TAT or TAT from other species) which have a desired sequence identity to the native TAT sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence TAT. By way of example, a screening method will comprise isolating the coding region of the TAT gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety

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of labels, including radionucleotides such as ³²P or ³⁵S, or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the TAT gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below. Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

Other useful fragments of the TAT-encoding nucleic acids include antisense or sense oligonucleotides comprising a singe-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target TAT mRNA (sense) or TAT DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of TAT DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. Such methods are encompassed by the present invention. The antisense oligonucleotides thus may be used to block expression of TAT proteins, wherein those TAT proteins may play a role in the induction of cancer in mammals. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugarphosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

Preferred intragenic sites for antisense binding include the region incorporating the translation initiation/start codon (5'-AUG / 5'-ATG) or termination/stop codon (5'-UAA, 5'-UAG and 5-UGA / 5'-TAA, 5'-TAG and 5'-TGA) of the open reading frame (ORF) of the gene. These regions refer to a portion of the mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation initiation or termination codon. Other preferred regions for antisense binding include: introns; exons; intron-exon junctions; the open reading frame (ORF) or "coding region," which is the region between the translation initiation codon and the translation termination codon; the 5' cap of an mRNA which comprises an N7-methylated guanosine residue joined to the 5'-most residue of the mRNA via a 5'-5' triphosphate linkage and includes 5' cap structure itself as well as the first 50 nucleotides adjacent to the cap; the 5' untranslated region (5'UTR), the portion of an mRNA in the 5' direction from the translation initiation codon, and thus including nucleotides between the 5' cap site and the translation initiation codon of an mRNA or corresponding nucleotides between the translation termination codon and 3' end of an mRNA or corresponding nucleotides between the translation termination codon and 3' end of an mRNA or corresponding nucleotides on the gene.

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Specific examples of preferred antisense compounds useful for inhibiting expression of TAT proteins include oligonucleotides containing modified backbones or non-natural internucleoside linkages. Oligonucleotides having modified backbones include those that retain a phosphorus atom in the backbone and those that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the art, modified oligonucleotides that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides. Preferred modified oligonucleotide backbones include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotri-esters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates, 5'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphorates, thionoalkylphosphotriesters, selenophosphates and borano-phosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein one or more internucleotide linkages is a 3' to 3', 5' to 5' or 2' to 2' linkage. Preferred oligonucleotides having inverted polarity comprise a single 3' to 3' linkage at the 3'-most internucleotide linkage i.e. a single inverted nucleoside residue which may be abasic (the nucleobase is missing or has a hydroxyl group in place thereof). Various salts, mixed salts and free acid forms are also included. Representative United States patents that teach the preparation of phosphorus-containing linkages include, but are not limited to, U.S. Pat. Nos.: 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563,253; 5,571,799; 5,587,361; 5,194,599; 5,565,555; 5,527,899; 5,721,218; 5,672,697 and 5,625,050, each of which is herein incorporated by reference.

Preferred modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; riboacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH.sub.2 component parts. Representative United States patents that teach the preparation of such oligonucleosides include, but are not limited to,. U.S. Pat. Nos.: 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; 5,792,608; 5,646,269 and 5,677,439, each of which is herein incorporated by reference.

In other preferred antisense oligonucleotides, both the sugar and the internucleoside linkage, i.e., the backbone, of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, an oligonucleotide mimetic

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that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative United States patents that teach the preparation of PNA compounds include, but are not limited to, U.S. Pat. Nos.: 5,539,082; 5,714,331; and 5,719,262, each of which is herein incorporated by reference. Further teaching of PNA compounds can be found in Nielsen et al., Science, 1991, 254, 1497-1500.

Preferred antisense oligonucleotides incorporate phosphorothioate backbones and/or heteroatom backbones, and in particular -CH₂-NH-O-CH₂-, -CH₂-N(CH₃)-O-CH₂- [known as a methylene (methylimino) or MMI backbone], -CH₂-O-N(CH₃)-CH₂-, -CH₂-N(CH₃)-N(CH₃)-CH₂- and -O-N(CH₃)-CH₂-CH₂- [wherein the native phosphodiester backbone is represented as -O-P-O-CH₂-] described in the above referenced U.S. Pat. No. 5,489,677, and the amide backbones of the above referenced U.S. Pat. No. 5,602,240. Also preferred are antisense oligonucleotides having morpholino backbone structures of the above-referenced U.S. Pat. No. 5,034,506.

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Modified oligonucleotides may also contain one or more substituted sugar moieties. Preferred oligonucleotides comprise one of the following at the 2' position: OH; F; O-alkyl, S-alkyl, or N-alkyl; Oalkenyl, S-alkeynyl, or N-alkenyl; O-alkynyl, S-alkynyl or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C $_1$ to C_{10} alkyl or C_2 to C_{10} alkenyl and alkynyl. Particularly preferred are $O[(CH_2)_nO]_mCH_3$, $O(CH_2)_nOCH_3$, $O(CH_2)_nNH_2$, $O(CH_2)_nCH_3$, $O(CH_2)_nONH_2$, and $O(CH_2)_nON[(CH_2)_nCH_3)]_2$, where n and m are from 1 to about 10. Other preferred antisense oligonucleotides comprise one of the following at the 2' position: C_1 to C_{10} lower alkyl, substituted lower alkyl, alkenyl, alkynyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH3, OCN, Cl, Br, CN, CF3, OCF3, SOCH3, SO2 CH3, ONO2, NO₂, N₃, NH₂, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. A preferred modification includes 2'-methoxyethoxy (2'-O-CH₂CH₂OCH₃, also known as 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin et al., Helv. Chim. Acta, 1995, 486-504) i.e., an alkoxyalkoxy group. A further preferred modification includes 2'-dimethylaminooxyethoxy, i.e., a O(CH₂)₂ON(CH₃)₂ group, also known as 2'-DMAOE, as described in examples hereinbelow, and 2'-dimethylaminoethoxyethoxy (also known in the art as 2'-O-dimethylaminoethoxyethyl or 2'-DMAEOE), i.e., 2'-O-CH₂-O-CH₂-N(CH₂).

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A further preferred modification includes Locked Nucleic Acids (LNAs) in which the 2'-hydroxyl group is linked to the 3' or 4' carbon atom of the sugar ring thereby forming a bicyclic sugar moiety. The linkage is preferably a methelyne (-CH₂-)_n group bridging the 2' oxygen atom and the 4' carbon atom wherein n is 1 or 2. LNAs and preparation thereof are described in WO 98/39352 and WO 99/14226.

Other preferred modifications include 2'-methoxy (2'-O-CH₃), 2'-aminopropoxy (2'-OCH₂CH₂CH₂CH

NH₂), 2'-allyl (2'-CH₂-CH=CH₂), 2'-O-allyl (2'-O-CH₂-CH=CH₂) and 2'-fluoro (2'-F). The 2'-modification may be in the arabino (up) position or ribo (down) position. A preferred 2'-arabino modification is 2'-F. Similar modifications may also be made at other positions on the oligonucleotide, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Oligonucleotides may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative United States patents that teach the preparation of such modified sugar structures include, but are not limited to, U.S. Pat. Nos.: 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; 5,792,747; and 5,700,920, each of which is herein incorporated by reference in its entirety.

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Oligonucleotides may also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl ($-C = C - CH_3$ or $-CH_2 - C = CH$) uracil and cytosine and other alkynyl derivatives of pyrimidine bases, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 2-F-adenine, 2-amino-adenine, 8-azaguanine and 8-azaguanine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Further modified nucleobases include tricyclic pyrimidines such as phenoxazine cytidine(1H-pyrimido[5,4-b][1,4]benzoxazin-2(3H)-one), phenothiazine cytidine (1H-pyrimido[5,4-b][1,4]benzothiazin-2(3H)-one), G-clamps such as a substituted phenoxazine cytidine 9-(2-aminoethoxy)-H-pyrimido[5,4-b][1,4]benzoxazin-2(3H)-one), (e.g. carbazole cytidine (2H-pyrimido[4,5-b]indol-2-one), pyridoindole cytidine (H-pyrido[3',2':4,5]pyrrolo[2,3-d]pyrimidin-2-one). Modified nucleobases may also include those in which the purine or pyrimidine base is replaced with other heterocycles, for example 7-deaza-adenine, 7-deazaguanosine, 2-aminopyridine and 2-pyridone. Further nucleobases include those disclosed in U.S. Pat. No. 3,687,808, those disclosed in The Concise Encyclopedia Of Polymer Science And Engineering, pages 858-859, Kroschwitz, J. I., ed. John Wiley & Sons, 1990, and those disclosed by Englisch et al., Angewandte Chemie, International Edition, 1991, 30, 613. Certain of these nucleobases are particularly useful for increasing the binding affinity of the oligomeric compounds of the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2.degree. C. (Sanghvi et al, Antisense Research and Applications, CRC Press, Boca Raton, 1993, pp. 276-278) and are preferred base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications. Representative United States patents

that teach the preparation of modified nucleobases include, but are not limited to: U.S. Pat. No. 3,687,808, as well as U.S. Pat. Nos.: 4,845,205; 5,130,302; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121, 5,596,091; 5,614,617; 5,645,985; 5,830,653; 5,763,588; 6,005,096; 5,681,941 and 5,750,692, each of which is herein incorporated by reference.

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Another modification of antisense oligonucleotides chemically linking to the oligonucleotide one or more moieties or conjugates which enhance the activity, cellular distribution or cellular uptake of the oligonucleotide. The compounds of the invention can include conjugate groups covalently bound to functional groups such as primary or secondary hydroxyl groups. Conjugate groups of the invention include intercalators, reporter molecules, polyamines, polyamides, polyethylene glycols, polyethers, groups that enhance the pharmacodynamic properties of oligomers, and groups that enhance the pharmacokinetic properties of oligomers. Typical conjugates groups include cholesterols, lipids, cation lipids, phospholipids, cationic phospholipids, biotin, phenazine, folate, phenanthridine, anthraquinone, acridine, fluoresceins, rhodamines, coumarins, and dyes. Groups that enhance the pharmacodynamic properties, in the context of this invention, include groups that improve oligomer uptake, enhance oligomer resistance to degradation, and/or strengthen sequence-specific hybridization with RNA. Groups that enhance the pharmacokinetic properties, in the context of this invention, include groups that improve oligomer uptake, distribution, metabolism or excretion. Conjugate moieties include but are not limited to lipid moieties such as a cholesterol moiety (Letsinger et al., Proc. Natl. Acad. Sci. USA, 1989, 86, 6553-6556), cholic acid (Manoharan et al., Bioorg. Med. Chem. Let., 1994, 4, 1053-1060), a thioether, e.g., hexyl-S-tritylthiol (Manoharan et al., Ann. N.Y. Acad. Sci., 1992, 660, 306-309; Manoharan et al., Bioorg. Med. Chem. Let., 1993, 3, 2765-2770), a thiocholesterol (Oberhauser et al., Nucl. Acids Res., 1992, 20, 533-538), an aliphatic chain, e.g., dodecandiol or undecyl residues (Saison-Behmoaras et al., EMBO J., 1991, 10, 1111-1118; Kabanov et al., FEBS Lett., 1990, 259, 327-330; Svinarchuk et al., Biochimie, 1993, 75, 49-54), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethyl-ammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et al., Tetrahedron Lett., 1995, 36, 3651-3654; Shea et al., Nucl. Acids Res., 1990, 18, 3777-3783), a polyamine or a polyethylene glycol chain (Manoharan et al., Nucleosides & Nucleotides, 1995, 14, 969-973), or adamantane acetic acid (Manoharan et al., Tetrahedron Lett., 1995, 36, 3651-3654), a palmityl moiety (Mishra et al., Biochim. Biophys. Acta, 1995, 1264, 229-237), or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety. Oligonucleotides of the invention may also be conjugated to active drug substances, for example, aspirin, warfarin, phenylbutazone, ibuprofen, suprofen, fenbufen, ketoprofen, (S)-(+)-pranoprofen, carprofen, dansylsarcosine, 2,3,5-triiodobenzoic acid, flufenamic acid, folinic acid, a benzothiadiazide, chlorothiazide, a diazepine, indomethicin, a barbiturate, a cephalosporin, a sulfa drug, an antidiabetic, an antibacterial or an antibiotic. Oligonucleotide-drug conjugates and their preparation are described in U.S. patent application Ser. No. 09/334,130 (filed Jun. 15, 1999) and United States patents Nos.: 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717, 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802;

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5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025;

4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941, each of which is herein incorporated by reference.

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It is not necessary for all positions in a given compound to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single compound or even at a single nucleoside within an oligonucleotide. The present invention also includes antisense compounds which are chimeric compounds. "Chimeric" antisense compounds or "chimeras," in the context of this invention, are antisense compounds, particularly oligonucleotides, which contain two or more chemically distinct regions, each made up of at least one monomer unit, i.e., a nucleotide in the case of an oligonucleotide compound. These oligonucleotides typically contain at least one region wherein the oligonucleotide is modified so as to confer upon the oligonucleotide increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding affinity for the target nucleic acid. An additional region of the oligonucleotide may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular endonuclease which cleaves the RNA strand of an RNA: DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of oligonucleotide inhibition of gene expression. Consequently, comparable results can often be obtained with shorter oligonucleotides when chimeric oligonucleotides are used, compared to phosphorothioate deoxyoligonucleotides hybridizing to the same target region. Chimeric antisense compounds of the invention may be formed as composite structures of two or more oligonucleotides, modified oligonucleotides, oligonucleosides and/or oligonucleotide mimetics as described above. Preferred chimeric antisense oligonucleotides incorporate at least one 2' modified sugar (preferably 2'-O-(CH₂)₂-O-CH₃) at the 3' terminal to confer nuclease resistance and a region with at least 4 contiguous 2'-H sugars to confer RNase H activity. Such compounds have also been referred to in the art as hybrids or gapmers. Preferred gapmers have a region of 2' modified sugars (preferably 2'-O-(CH₂)₂-O-CH₃) at the 3'-terminal and at the 5' terminal separated by at least one region having at least 4 contiguous 2'-H sugars and preferably incorporate phosphorothioate backbone linkages. Representative United States patents that teach the preparation of such hybrid structures include, but are not limited to, U.S. Pat. Nos. 5,013,830; 5,149,797; 5,220,007; 5,256,775; 5,366,878; 5,403,711; 5,491,133; 5,565,350; 5,623,065; 5,652,355; 5,652,356; and 5,700,922,

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The antisense compounds used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including, for example, Applied Biosystems (Foster City, Calif.). Any other means for such synthesis known in the art may additionally or alternatively be employed. It is well known to use similar techniques to prepare oligonucleotides such as the phosphorothioates and alkylated derivatives. The compounds of the invention may also be admixed, encapsulated, conjugated or otherwise associated with other molecules, molecule structures or mixtures of compounds, as for example, liposomes, receptor targeted molecules, oral,

each of which is herein incorporated by reference in its entirety.

rectal, topical or other formulations, for assisting in uptake, distribution and/or absorption. Representative United States patents that teach the preparation of such uptake, distribution and/or absorption assisting formulations include, but are not limited to, U.S. Pat. Nos. 5,108,921; 5,354,844; 5,416,016; 5,459,127; 5,521,291; 5,543,158; 5,547,932; 5,583,020; 5,591,721; 4,426,330; 4,534,899; 5,013,556; 5,108,921; 5,213,804; 5,227,170; 5,264,221; 5,356,633; 5,395,619; 5,416,016; 5,417,978; 5,462,854; 5,469,854; 5,512,295; 5,527,528; 5,534,259; 5,543,152; 5,556,948; 5,580,575; and 5,595,756, each of which is herein incorporated by reference.

Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, CaPO 4-mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

Antisense or sense RNA or DNA molecules are generally at least about 5 nucleotides in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710,

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720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related TAT coding sequences.

Nucleotide sequences encoding a TAT can also be used to construct hybridization probes for mapping the gene which encodes that TAT and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

When the coding sequences for TAT encode a protein which binds to another protein (example, where the TAT is a receptor), the TAT can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor TAT can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native TAT or a receptor for TAT. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

Nucleic acids which encode TAT or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding TAT can be used to clone genomic DNA encoding TAT in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding TAT. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for TAT transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding TAT introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding TAT. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential

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therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of TAT can be used to construct a TAT "knock out" animal which has a defective or altered gene encoding TAT as a result of homologous recombination between the endogenous gene encoding TAT and altered genomic DNA encoding TAT introduced into an embryonic stem cell of the animal. For example, cDNA encoding TAT can be used to clone genomic DNA encoding TAT in accordance with established techniques. A portion of the genomic DNA encoding TAT can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, Cell, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., Cell, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the TAT polypeptide.

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Nucleic acid encoding the TAT polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve in vivo synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes in vivo. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik et al., Proc. Natl. Acad. Sci. USA 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

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There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells in vitro, or in vivo in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells in vitro include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred in vivo gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau

et al., <u>Trends in Biotechnology</u> 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu et al., <u>J. Biol. Chem.</u> 262, 4429-4432 (1987); and Wagner et al., <u>Proc. Natl. Acad. Sci. USA</u> 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson et al., <u>Science</u> 256, 808-813 (1992).

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The nucleic acid molecules encoding the TAT polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each TAT nucleic acid molecule of the present invention can be used as a chromosome marker.

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The TAT polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the TAT polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. TAT nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

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This invention encompasses methods of screening compounds to identify those that mimic the TAT polypeptide (agonists) or prevent the effect of the TAT polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the TAT polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins, including e.g., inhibiting the expression of TAT polypeptide from cells. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

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The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

All assays for antagonists are common in that they call for contacting the drug candidate with a TAT polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

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In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the TAT polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the TAT polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the TAT polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the

immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

If the candidate compound interacts with but does not bind to a particular TAT polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and coworkers (Fields and Song, Nature (London), 340:245-246 (1989); Chien et al., Proc. Natl. Acad. Sci. USA, 88:9578-9582 (1991)) as disclosed by Chevray and Nathans, Proc. Natl. Acad. Sci. USA, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "twohybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GALA, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1- lacZ reporter gene under control of a GAL4activated promoter depends on reconstitution of GALA activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β-galactosidase. A complete kit (MATCHMAKERTM) for identifying protein-protein interactions between two specific proteins using the twohybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

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Compounds that interfere with the interaction of a gene encoding a TAT polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

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To assay for antagonists, the TAT polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence

of the TAT polypeptide indicates that the compound is an antagonist to the TAT polypeptide. Alternatively, antagonists may be detected by combining the TAT polypeptide and a potential antagonist with membrane-bound TAT polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The TAT polypeptide can be labeled, such as by radioactivity, such that the number of TAT polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., Current Protocols in Immun., 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the TAT polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the TAT polypeptide. Transfected cells that are grown on glass slides are exposed to labeled TAT polypeptide. The TAT polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor.

As an alternative approach for receptor identification, labeled TAT polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro- sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA

library to identify the gene encoding the putative receptor.

In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled TAT polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with TAT polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the TAT polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the TAT polypeptide.

Another potential TAT polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature TAT polypeptides herein, is used to design an antisense

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RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al., Science, 241: 456 (1988); Dervan et al., Science, 251:1360 (1991)), thereby preventing transcription and the production of the TAT polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into the TAT polypeptide (antisense - Okano, Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, FL, 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed in vivo to inhibit production of the TAT polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

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Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the TAT polypeptide, thereby blocking the normal biological activity of the TAT polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

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Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Ross<u>Current Biology</u>, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

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Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, supra.

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These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

Isolated TAT polypeptide-encoding nucleic acid can be used herein for recombinantly producing TAT polypeptide using techniques well known in the art and as described herein. In turn, the produced TAT polypeptides can be employed for generating anti-TAT antibodies using techniques well known in the art and as described herein.

Antibodies specifically binding a TAT polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders, including cancer, in the form of pharmaceutical compositions.

If the TAT polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, e.g., Marasco et al., Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993).

The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

20 EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

EXAMPLE 1: Analysis of Differential TAT Polypeptide Expression by GEPIS

An expressed sequence tag (EST) DNA database (LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) was searched and interesting EST sequences were identified by GEPIS. Gene expression profiling in silico (GEPIS) is a bioinformatics tool developed at Genentech, Inc. that characterizes genes of interest for new cancer therapeutic targets. GEPIS takes advantage of large amounts of EST sequence and library information to determine gene expression profiles. GEPIS is capable of determining the expression profile of a gene based upon its proportional correlation with the number of its occurrences in EST databases, and it works by integrating the LIFESEQ® EST relational database and Genentech proprietary information in a stringent and statistically meaningful way. In this example, GEPIS is used to identify and cross-validate novel tumor antigens, although GEPIS can be configured to perform either very specific analyses or broad screening tasks. For the initial screen, GEPIS is used to identify EST sequences from the LIFESEQ® database that correlate

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to expression in a particular tissue or tissues of interest (often a tumor tissue of interest). Then, GEPIS was employed to generate a complete tissue expression profile for the various sequences of interest. Using this type of screening bioinformatics, various TAT polypeptides (and their encoding nucleic acid molecules) were identified as being significantly overexpressed in a particular type of cancer or certain cancers as compared to other cancers and/or normal non-cancerous tissues. The rating of GEPIS hits is based upon several criteria including, for example, tissue specificity, tumor specificity and expression level in normal essential and/or normal proliferating tissues. The following is a list of molecules whose tissue expression profile as determined by GEPIS evidences significant upregulation of expression in a specific tumor or tumors as compared to other tumor(s) and/or normal tissues and optionally relatively low expression in normal essential and/or normal proliferating tissues.

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Under each tissue heading shown below is a list of the cDNA sequences that are detectably overexpressed in tumor tissue of the indicated tissue type as compared to normal non-tumor tissue of the same tissue type. As such, the molecules listed below (and the polypeptides they encode) are excellent nucleic acid (and polypeptide) targets for the diagnosis and therapy of cancer in mammals.

15	PERIPHERAL NERVOUS SYSTEM					
	DNA324303	DNA324573	DNA324681	DNA325296	DNA325405	DNA325407
	DNA325408	DNA325409	DNA325410	DNA325449	DNA325503	DNA326083
	DNA326231	DNA188229	DNA327080	DNA327081	DNA327082	
20	<u>BRAIN</u>					
	DNA323721	DNA323722	DNA323723	DNA323724	DNA323726	DNA323727
	DNA323728	DNA323729	DNA323731	DNA323732	DNA287173	DNA151148
	DNA323740	DNA323742	DNA323743	DNA323744	DNA323751	DNA323753
	DNA323755	DNA323757	DNA323759	DNA323764	DNA323765	DNA323778
25	DNA323781	DNA323783	DNA323785	DNA323795	DNA323796	DNA323797
	DNA323805	DNA323810	DNA323811	DNA323812	DNA323814	DNA83085
	DNA323817	DNA323821	DNA273060	DNA323823	DNA323824	DNA256503
	DNA323825	DNA323826	DNA323828	DNA323829	DNA323830	DNA323833
	DNA103214	DNA323834	DNA323837	DNA323838	DNA323839	DNA323846
30	DNA323856	DNA323859	DNA323863	DNA323869	DNA323871	DNA323874
	DNA323882	DNA323887	DNA323888	DNA323892	DNA323893	DNA323897
	DNA323898	DNA323900	DNA323901	DNA323902	DNA323908	DNA210134
	DNA323912	DNA323918	DNA323921	DNA323922	DNA323923	DNA323924
	DNA323925	DNA323926	DNA257916	DNA323927	DNA323931	DNA323936
35	DNA323937	DNA323938	DNA323939	DNA323940	DNA323942	DNA226793
	DNA294794	DNA323943	DNA323944	DNA323946	DNA323947	DNA323950